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(54) Title: RECOMBINANT PEPTIDES DERIVED FROM THE Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES

(57) Abstract

The present invention provides recombinant peptides that specifically and selectively bind to the human milk fat globule (HMFG) antigen, BA46. In particular, the present invention provides recombinant variants of the Mc3 antibody, including humanized versions of Mc3. The variant Mc3 peptides are particularly useful for diagnostic, prognostic, and therapeutic applications in the field of breast cancer. The present invention also provides methods for the humanization of antibodies such as murine monoclonal antibodies. The novel humanization methods are applied to the production of humanized Mc3 antibodies and it is shown that these humanized antibodies retain the ability to engage in high affinity binding to their cognate antigen. Such humanization enables the use of these antibodies for immunodiagnostic and immunotherapeutic applications in humans.

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RECOMBINANT PEPTIDES DERIVED FROM THE Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES

Technical Field

This invention relates to the diagnosis and therapy of neoplastic tumors, particularly human breast carcinomas, as well as the field of protein engineering particularly the humanization of antibodies.

Background

The human milk fat globule (HMFG) can be used as a source of antigenic material for the preparation of both polyclonal and monoclonal antibodies for use in the diagnosis and treatment of breast cancer, as well as in the study of the breast epithelial cell surface and the processing of its antigenic components.

The milk fat globule membrane is derived from the apical surface of the mammary epithelial cell during lactation (Patton, S., et al. (1975) *Biochim Biophys Acta* **415**: 273-309). As a result, the HMFG, has been a source for isolation of breast membrane glycoproteins (Taylor, P.J., et al. (1981) *Int J Cancer* **28**: 17-21). Using the HMFG membrane as an immunogen, polyclonal antisera were prepared that proved to have specificity for breast epithelial cells after absorption with non-breast tissue. These polyclonal antisera specifically bound three glycoproteins of molecular weights of 150, 70, and 46 kDa, respectively (Ceriani, R.L., et al. (1977) *Proc Natl Acad Sci U S A* **74**: 582-6).

Monoclonal antibodies against the HMFG have been used in the identification of a novel component of the breast epithelial cell surface, a large molecular weight mucin-like glycoprotein, that was named non-penetrating

glycoprotein or NPGP (Peterson, J.A., et al. (1990) *Hybridoma* **9**: 221-35; and Ceriani, R.L., et al. (1983) *Somatic Cell Genet* **9**: 415-27). This molecule has been used as a target in breast cancer radioimmunotherapy (Kramer, E.L., et al. (1993) *J Nucl Med* **34**: 1067-74; and Ceriani, R.L., et al. (1988) *Cancer Res* **48**: 4664-72), in the development of a serum assay for breast cancer diagnosis (Ceriani, R.L., et al. (1982) *Proc Natl Acad Sci U S A* **79**: 5420-4; and Ceriani, R.L., et al. (1992) *Anal Biochem* **201**: 178-84), and in breast cancer prognosis using immunohistochemistry (Ceriani, R.L., et al. (1992) *Int J Cancer* **51**: 343-54). This non-penetrating glycoprotein (NPGP) appears to be extremely antigenic in mice. The vast majority of monoclonal antibodies prepared against HMFG as well as breast tumors have been found to have specificity against different epitopes of this mucin.

However, the smaller molecular weight proteins of the HMFG also appear to be important surface markers for breast epithelial cells. The 46 kDa and 70 kDa HMFG antigens are also found in the serum of breast cancer patients and thus can be used as markers for breast cancer in serum assays. In addition, the 70 kDa component has been found to co-purify with the intact NPGP complex and has been shown to be linked to NPGP by disulfide bonds.

Few monoclonal antibodies, however, have been prepared against the smaller components of the human milk fat globule system, such as the 70 kDa and 46 kDa HMFG antigens. Although, Peterson, J.A., et al. (1990) *Hybridoma* **9**: 221-35 were able to generate a group of monoclonal antibodies against HMFG that did detect the 46 kDa HMFG antigen, including the Mc3 antibody. The 46 kDa component of the HMFG system, also known as BA46, has been found to be present in the serum of breast cancer patients (Salinas, F.A., et al. (1987) *Cancer Res* **47**: 907-13), and an increase in circulating BA46 was found to be associated with increased tumor burden. In addition, BA46 has been a target molecule in experimental radioimmunotherapy of transplanted human breast tumors in nude mice (Ceriani, R.L. et al. (1988) *Cancer Res* **48**: 4664-72).

In some breast carcinomas, there is an over-expression of the BA46 antigen (Larocca, D., et al. (1991) *Cancer Res* **51**: 4994-8). Also, in human milk BA46 appears to have anti-rotavirus activity that may involve binding to rotavirus

(Yolken, R.H., et al. (1992) *J Clin Invest* **90**: 1984-91) and that may interfere with viral infections in newborns.

A partial cDNA sequence of BA46 has been previously reported (Larocca, D., et al. (1991) *Cancer Res* **51**: 4994-8) that placed BA46 in a family of proteins possessing factors V/VIII C1/C2-like domains related to discoidin I (Johnson, J.D., et al. (1993) *Proc Natl Acad Sci U S A* **90**: 5677-81). BA46's closest relatives may be found among the murine MGF-E8 (Stubbs, J.D., et al. (1990) *Proc Natl Acad Sci U.S.A.* **87**: 8417-21), the bovine components 15/16 (Mather, I.H., et al. (1993) *Biochem Mol Biol Int* **29**: 545-54) and the guinea-pig GP55 (Mather, I.H., et al. (1993) *Biochem Mol Biol Int* **29**: 545-54) proteins.

cDNA cloning and *in vitro* cell adhesion studies, provide evidence that BA46 is a breast epithelial cell membrane glycoprotein involved in intercellular interactions. BA46 is localized to the membrane fraction when isolated from breast carcinoma cells (Larocca, D., et al. (1991) *Cancer Res* **51**: 4994-8). BA46 most likely interacts with membrane integrins via its RGD containing EGF-like domain.

Carcinomas result from the carcinogenic transformation of cells of different epithelia. Two of the most damaging characteristics of carcinomas are their uncontrolled growth and their ability to create metastases in distant sites of the host, particularly a human host. It is usually these distant metastases that cause serious consequences to the host, since frequently the primary carcinoma may usually be removed by surgery. The treatment of metastatic carcinomas, that are seldom removable, depends on irradiation therapy and systemic therapies of different natures. The systemic therapies currently include, chemotherapy, radiation, hormone therapy, immunity-boosting pharmaceutical agents and procedures, hyperthermia and systemic monoclonal antibody treatment. In the latter case the antibody proteins can be labeled with radioactive elements, immunotoxins and chemotherapeutic drugs.

Radioactively labeled monoclonal antibodies were initially used with success in lymphomas and leukemia, and recently in some carcinomas. The concept underlying the use of labeled antibodies is that the labeled antibody will specifically seek and bind to the carcinoma and the radioactive element will irradiate the tumor *in situ*. Since the particles discharged during radioactive decay travel some distance

through the tumors it is not necessary that every carcinoma cell bind the labeled antibody. The specificity of the monoclonal antibodies permit the selective treatment of the tumor while avoiding the irradiation of non-malignant tissues. The use of systemic radiation and chemotherapeutic agents without targeting agents produce serious toxic side effects in normal, nonmalignant tissues, making these therapies undesirable for carcinomas and the use of radiolabeled monoclonal antibodies a valid alternative.

Antibodies raised against human epitopes have been used for the diagnosis and therapy of carcinomas. Also known are methods for preparing both polyclonal and monoclonal antibodies. Examples of the latter are BrE-2, BrE-3 and KC-4 (e.g., US patent Nos. 5,077,220; 5,075,219 and 4,708,930).

Summary of the Invention

The present invention provides recombinant peptides that specifically and selectively bind to the human milk fat globule (HMFG) antigen, BA46. In particular, the present invention provides recombinant variants of the Mc3 antibody, including humanized versions of Mc3. The variant Mc3 peptides are particularly useful for diagnostic, prognostic, and therapeutic applications in the field of breast cancer.

The present invention also provides methods for the humanization of antibodies such as murine monoclonal antibodies. The novel humanization methods are applied to the production of humanized Mc3 antibodies and it is shown that these humanized antibodies retain the ability to engage in high affinity binding to their cognate antigen. Such humanization enables the use of these antibodies for immunodiagnostic and immunotherapeutic applications in humans.

A number of the preferred embodiments of the present invention are enumerated below.

1. A recombinant Mc3 antibody which binds to BA46 antigen of the human milk fat globule (HMFG), said antibody comprising at least one modified variable region, said modified variable region selected from the group consisting of: (i) a modified heavy chain variable region having an amino acid sequence substantially

similar to that of murine Mc3 in Figure 12 in which at least one but fewer than about 30 of the amino acid residues of murine Mc3 have been substituted; and (ii) a modified light chain variable region having an amino acid sequence substantially similar to that of murine Mc3 in Figure 13 in which at least one but fewer than about 30 of the amino acid residues of murine Mc3 have been substituted; and (iii) a derivative of one of said modified variable regions in which one or more residues of the variable region that are not required for binding to the antigen have been deleted or in which one of more of the residues labelled (CDR) in Figure 12 or 13 have been modified without disrupting antigen binding. Preferably, there are between about 3 and 25 substitutions, more preferably between about 5 and 20, still more preferably between about 7 and 17. Preferably, such modifications result in the humanization of the recombinant Mc3 variable regions; more preferably the variable regions are humanized according to the buried-residue-modification technique, as described below. Residues within the CDR can also be modified (substituted, deleted, or added to) so long as these modifications do not substantially disrupt antigen binding. Preferably, all of the Mc3 variants of the present invention retain a level of avidity that is at least about 20% that of the starting antibody (i.e. the murine Mc3), more preferably at least about 40%, still more preferably at least about 60%, still more preferably at least about 80%, most preferably at least about 90%. The term "recombinant" refers to the fact that the antibodies of the present invention are not naturally occurring and are the products of recombinant techniques.

2. A recombinant murine Mc3 antibody of embodiment 1, wherein at least one of said substituted amino acids is replaced with the corresponding amino acid from the appropriate human consensus sequence of Figure 12 or 13, for a heavy or light chain variable region, respectively. Non-consensus but commonly observed human residues can also be used, but consensus residues are the most preferred.

3. A recombinant Mc3 antibody of embodiment 1 wherein said antibody comprises a heavy chain variable region and a light chain variable region.

4. A recombinant Mc3 antibody of embodiment 3 wherein both variable regions are modified variable regions, and wherein the antibody further comprises

an antibody constant region or other effector agent. Any of a variety of effector agents can be joined to the antibodies of the present invention, as described below.

5. A recombinant Mc3 antibody of embodiment 4 wherein the antibody comprises a constant region that is a human antibody constant region.

6. A recombinant Mc3 antibody of embodiment 1 wherein at least about five of the amino acid residues in one of said modified variable regions have been replaced with corresponding amino acids from the appropriate human consensus sequence of Figure 12 or 13, for a heavy or light chain variable region, respectively.

7. A recombinant Mc3 antibody of embodiment 1 comprising a modified heavy chain variable region in which at least about half of the residues listed as humanized or humanized (BR) in Figure 12 have been replaced with corresponding residues from the human consensus sequence of Figure 12.

8. A recombinant Mc3 antibody of embodiment 1 comprising a modified light chain variable region in which at least about half of the residues listed as humanized or humanized (BR) in Figure 13 have been replaced with corresponding residues from the human consensus sequence of Figure 13.

9. A recombinant Mc3 antibody of embodiment 5 comprising a modified heavy chain variable region in which at least about 90% of the residues listed as humanized or humanized (BR) in Figure 12 have been replaced with corresponding residues from the human consensus sequence of Figure 12; and a modified light chain variable region in which at least about 90% of the residues listed as humanized or humanized (BR) in Figure 13 have been replaced with corresponding residues from the human consensus sequence of Figure 13.

10. A recombinant Mc3 antibody of embodiment 9 in which all of the residues listed as humanized or humanized (BR) have been replaced with corresponding residues from the human consensus sequences of Figures 12 or 13, for the heavy and light chains respectively.

11. A pharmaceutical composition comprising a recombinant Mc3 antibody of embodiment 1 and a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers are well known in the art. See, e.g., Remington's Pharmaceutical Sciences, Mack Publ., Easton, PA.

12. A nucleic acid sequence encoding a modified variable region of embodiment 1.

13. A nucleic acid sequence of embodiment 12 comprising the coding region of a modified variable region as shown in Figure 18 or 19. Coding regions are those shown in capital letters.

14. An in vitro method of detecting the presence of an HMFG antigen or binding fragment thereof, comprising obtaining a biological sample suspected of comprising the antigen or a fragment thereof; adding a recombinant Mc3 antibody of embodiment 1 under conditions effective to form an antibody-antigen complex; and detecting the presence of said antibody-antigen complex.

15. A method of diagnosing the presence of an HMFG antigen or binding fragment thereof in a subject, comprising administering to the subject a recombinant Mc3 antibody of embodiment 1 under conditions effective to deliver it to an area of the subject's body suspected of containing an HMFG antigen or a binding fragment thereof to form an antibody-antigen complex; and detecting the presence of said antibody-antigen complex.

16. A method of delivering an agent to a target site that contains an HMFG antigen comprising binding said agent to a recombinant Mc3 antibody of embodiment 1 at a position other than the antigen binding site to create an agent-antibody complex; and introducing the agent-antibody complex to the environment of said target site under conditions suitable for binding of an antibody to its cognate antigen.

17. A method of embodiment 16, wherein the target site is within the body of a human subject and introducing the agent-antibody complex comprises administering the complex to said subject.

18. A method of humanizing a non-human antibody comprising replacing one or more framework amino acid residues in a variable region of said antibody with corresponding framework amino acids from a human variable region wherein important non-human framework residues, as defined by the buried-residue-modification technique, are retained in their original form. The buried-residue-modification technique is described below.

19. A method of humanizing a non-human antibody comprising replacing one or more framework amino acid residues in a variable region of said antibody with corresponding framework amino acids from a human variable region consensus sequence wherein important non-human framework residues, as defined by the buried-residue-modification technique, are retained in their original form.

20. A method of embodiment 19 wherein both the heavy and the light chain variable regions of said antibody are humanized. Such modified variable regions are preferably joined to corresponding constant regions derived from a human antibody. Other effector agents may also be joined as described below.

Brief Description of the Drawings

Figure 1 illustrates Fab structures for which coordinates are available in the Protein Data Bank.

Figure 2 and 3 illustrate V_L and V_H framework residues, respectively, that contact CDR residues in Fabs of known three-dimensional structure.

Figure 4 illustrates framework residues that contact framework residues in the opposite domain in Fabs of known three-dimensional structure.

Figures 5 and 6 illustrate buried framework residues in the V_L and V_H regions, respectively, of Fabs of known three-dimensional structure.

Figure 7 illustrates human antibodies that are most similar in sequence to murine antibodies of known three-dimensional structure.

Figure 8 (SEQ ID NO:1 through SEQ ID NO:18) and 9 (SEQ ID NO:19 through SEQ ID NO:45) illustrate framework residues in V_L and V_H, respectively, that probably need to be preserved in order to reproduce the ligand-binding properties of the original antibody.

Figures 10 (SEQ ID NO:46 and SEQ ID NO:47)and 11 (SEQ ID NO:48 and SEQ ID NO:49) illustrate the nucleotide sequences and corresponding amino acid sequences of the V_H and V_L regions, respectively, of Mc3 and their respective leader peptides. Nucleotides and amino acids are shown as the standard one letter codes. Lower case amino acids represent the leader peptides. Lower case nucleotides represent primer sequence overlaps and may, therefore, not correspond to the natural sequences.

Figures 12 and 13 illustrate the humanization protocol (buried-residue-modification technique) used to modify the V_H and V_L regions, respectively, of the Mc3 antibody.

Figures 14 (SEQ ID NO:47)and 15 (SEQ ID NO:49) illustrate the amino acid sequences of the V_H and V_L regions of the Mc3 antibody, respectively, humanized according to the buried-residue-retention technique.

Figures 16 (SEQ ID NO:50 through SEQ ID NO:55)and 17(SEQ ID NO:56 through SEQ ID NO:61) illustrate primers used in the construction of genes encoding humanized Mc3 antibody (HuMc3).

Figures 18 (SEQ ID NO:62 and SEQ ID NO:63) and 19 (SEQ ID NO:64 and SEQ ID NO:65) illustrate the nucleotide and derived protein sequences of the V_H and V_L regions, respectively, of HuMc3v2.

Figure 20 illustrates the results of a competition assay between MuMc3 (wild-type murine Mc3 antibody) or HuMc3 (humanized Mc3 antibody) and ^{125}I-MuMc3.

Figure 21 illusrates the results of biodistribution studies in nude mice bearing the human MX-1 transplantable breast tumor, showing the location of ^{125}I-labeled control IgG, MuMc3, and HuMc3 at 1, 2, 4, and 8 days after injection.

Figure 22 illustrates the results of radioimmunotherapy studies in mice bearing the MX-1 tumor. ^{131}I-labeled HuMc3 contained or reduced tumor mass in treated animals, while the tumor in untreated animals grew to ~20 times the original size.

Figure 23 illustrates the results of biodistribution studies in mice bearing the MX-1 tumor, in which MuMc3 and HuMc3 was radiolabeled with ^{111}In using the chelator MXDTPA.

Detailed Description of the Invention

The Mc3 antibody offers considerable promise for use in the immunodetection and immunotherapy of breast cancer. It is known that Mc3 binds to the BA-46 antigen in the human milk fat globule. See R. Ceriani et al., Proc. Natl. Acad. Sci. 79:5420-5424 (1982); R. Ceriani et al., Somatic Cell Genetics 9:415-427 (1983); R. Ceriani and E. Blank, Cancer Res. 48:4664-4672 (1988); and J. Peterson et al., Hybridoma 9:221-235 (1990). See also International Publication

WO92/07939, published May 14, 1992, by Ceriani & Peterson (describing the BA-46 antigen).

Recombinant variants of the Mc3 monoclonal antibody would be especially useful in order to provide a variety of Mc3-related immunodiagnostic and immunotherapeutic agents. A particularly desirable class of such variants are "humanized" Mc3 derivatives that retain the ability to interact with HMFG antigen BA-46 with high specificity and avidity; but exhibit reduced immunogenicity in humans. However, without knowing the amino acid sequences of the Mc3 antibody chains (in particular the variable regions thereof) and without having DNA sequences available, it is not feasible to develop such variants.

As described below, the present inventors have cloned and sequenced the critical regions of the Mc3 antibody, and have now described and enabled a variety of Mc3 variant peptides.

In addition, as described below, the present inventors have developed a new humanization technique for preparing antibody variants in which the tendency to elicit a human anti-mouse antibody (HAMA) reaction in humans is drastically reduced or eliminated. Using Mc3 as a first illustration, the technique has resulted in the generation of an especially preferred class of humanized Mc3 variants in which particular amino acid residues in the framework region of the variable chain have been selectively humanized. It has been shown that these humanized Mc3 variants remained quite effective at binding to their cognate antigen.

Preparing Recombinant Peptides of Mc3

The present inventors selected the following strategy for the preparation and manufacture of the recombinant and hybrid peptides of this invention. The cDNAs that encode the antibody variable regions, V_L and V_H, of the light and heavy chains respectively can be obtained by isolation of mRNA from a hybridoma cell and reverse transcription of the mRNA, amplification of the cDNA by polymerase chain reaction (PCR) and insertion of the DNA into a vector for optional sequencing, and for restriction enzyme cutting. In general, both the V_L and V_H variable regions are required to effectively reproduce the binding properties of an antibody. There are two closely related kinds of V_L regions (depending on whether

the V_L is derived from the kappa or the lambda light chain) and these are further subdivided by convention into several sequence families (see Kabat et al. 1991). There are also several sequence families for V_H (id.).

The variable region cDNAs can then be modified with predesigned primers used to PCR amplify them or synthesized de novo, cloned into a vector optionally carrying DNA sequences encoding, e.g., constant region(s), optionally sequenced, and then transfected into a host cell for expression of the recombinant gene product. The binding specificity characteristics of the recombinant peptides may then be determined and compared to those of the originally isolated antibodies.

Having the sequence available, one can apply any of a number of techniques to the production of variants of the Mc3 antibody that retain antigen binding but exhibit other features that make them more desirable for particular diagnostic and/or therapeutic uses. An especially preferred class of such variants described herein are humanized variants in which the variable regions of the light and/or heavy chains have been modified to make them less likely to elicit any immunogenic (HAMA) response in humans. Such variants are thus more useful for in vivo administration. While several different humanization protocols can be utilized, as described herein, we have developed a new technique for antibody humanization that is especially useful because it achieves two highly desirable but frequently conflicting goals: (i) humanizing as many residues as possible to reduce the likelihood of immunogenicity; and (ii) retaining the avidity of the original heterologous antibody.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, MOLECULAR CLONING: A LABORATORY MANUAL, Second Edition (1989), OLIGONUCLEOTIDE SYNTHESIS (M.J. Gait Ed., 1984), ANIMAL CELL CULTURE (R.I. Freshney, Ed., 1987), the series METHODS IN ENZYMOLOGY (Academic Press, Inc.); GENE TRANSFER VECTORS FOR MAMMALIAN CELLS (J.M. Miller and M.P. Calos Eds. 1987), HANDBOOK OF EXPERIMENTAL IMMUNOLOGY, (D.M. Weir and C.C. Blackwell, Eds.);

CELLULAR AND MOLECULAR IMMUNOLOGY, (A.K. Abbas, A.H. Lichtman and J.S. Pober, 1991 and 1993); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, (F.M. Ausubel, R. Brent, R.E. Kingston, D.D. Moore, J.G. Siedman, J.A. Smith, and K. Struhl Eds. 1987 and 1993); and CURRENT PROTOCOLS IN IMMUNOLOGY (J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach and W. Strober Eds. 1991).

All patents, patent applications, and publications mentioned herein, both supra and infra, are hereby incorporated herein by reference.

By way of illustrating both the potential use of the variant antibodies described herein, and the significance of expanding their utility via humanization, one can consider the use of radioimmunoconjugates of such antibodies in both diagnostic and therapeutic applications. As an example, BrE-3 antibodies (Peterson et al. (1990) *Hybridoma* **9**: 221; and U.S. Patent No. 5,075,219 by Ceriani & Peterson) are known to bind preferentially to neoplastic carcinoma tumors because the tumors express an unglycosylated form of the breast epithelial mucin that is not expressed in normal epithelial tissue. This preferential binding combined with an observed low concentration of epitope for these antibodies in the circulation of carcinoma patients, such as breast cancer patients, makes antibodies having specificity for a mucin epitope a potentially effective carcinoma radioimmunotherapy. A ^{90}Y-BrE-3 radioimmunoconjugate proved highly effective against human breast carcinomas transplanted into nude mice. Human clinical studies showed the ^{90}Y-BrE-3 radioimmunoconjugate to considerably reduce the size of breast tumor metastases without any immediate toxic side effects. Moreover, an ^{111}In-BrE-3 radioimmunoconjugate was successfully used for imaging 15 breast cancer patients, providing excellent tumor targeting in 13 out of 15 of the patients. Out of all the breast tumor metastases occurring in another study, 86% were detected by ^{111}In-BrE-3. Unfortunately, 2 to 3 weeks after treatment, the patients developed a strong human anti-murine antibody (HAMA) response that prevented further administration of the radioimmunoconjugate. The HAMA response, which is observed for numerous murine monoclonal antibodies, precludes any long-term administration of murine antibodies to human patients.

Similarly, other heterologous antibodies, when administered to humans, elicited similar antibody responses. The anti-heterologous human response is thus a substantial factor limiting the successful use of heterologous monoclonal antibodies as therapeutic agents.

Antibody Humanization

Based on the studies described above and others, it is apparent that in many cases monoclonal antibodies can only be administered once to a subject because of the detrimental effects of eliciting an immunogenic response. This is true for most heterologous antibodies being administered to mammalian animals.

Several different attempts have been made in an effort to circumvent these problems, including the development of so-called "chimeric antibodies" and "CDR-grafted antibodies", and attempts to generate human monoclonal hybridoma lines. These efforts have met with only limited success. "Chimeric antibodies" are direct fusions between variable domains of one species and constant domains of another. Murine/human chimeric antibodies have been shown to be less immunogenic in humans than whole murine antibodies, but, nevertheless, in some cases an immune response is mounted to the murine variable region. A further reduction of the "foreign" or heterologous nature of antibodies was achieved by "grafting" only the CDRs. from a murine monoclonal antibody onto a human supporting framework (i.e. the framework region or "FR") prior to its subsequent fusion with an appropriate constant domain, (European Patent Application, Publication No. 239,400 to Winter; Riechmann, et al. (1988) *Nature* **332**: 323-327). However, the procedures employed to accomplish CDR-grafting can yield "humanized" antibodies that are not as effective at binding to the antigen. That is, the resultant CDR-grafted antibodies have tended to lose avidity (in many cases to less than one third of the original avidity). The third type of technique, use of human monoclonal hybridoma lines have also not been generally satisfactory. In particular, human monoclonal hybridoma cell lines have not been very stable and have, therefore, not been suitable for the large scale, repeated production of monoclonal antibodies.

An improved technique for the humanization of monoclonal antibodies is described in International Publication WO94/11509, published May 26, 1994, by

Couto et al. That technique, referred to herein as the "buried-residue-retention technique" or "BR-R technique", is also described below.

A further improved technique for the humanization of monoclonal antibodies is described herein. Using this novel technique, referred to as the "buried-residue-modification technique" or "BR-M technique", we have produced humanized Mc3 peptides, as described below. Surprisingly, while the buried-residue-modification technique involved the humanization of even more residues than the earlier-described BR-R technique, and is thus expected to further reduce the possibility of eliciting a HAMA response in humans, the resulting humanized Mc3 antibody variant has been shown to retain substantially all of the avidity of the original murine antibody. A description of these techniques and illustrative applications are provided below.

As a general matter, the ligand binding characteristics of an antibody combining site are determined primarily by the structure and relative disposition of the CDRs, although some neighboring residues also have been found to be involved in antigen binding (Davies, et al. (1990) *Ann. Rev. Biochem.* **59**: 439-473). The humanized derivatives of non-human antibodies rely to varying degrees upon the complementary determining regions (CDRs) to provide binding affinity to the antibody's ligand, and the framework residues (FRs) which support the CDRs to dictate their disposition relative to one another. The crystallographic analysis of numerous antibody structures has revealed that the antigen/antibody binding site is composed almost entirely of the CDR residues. The necessity of the CDRs to form these structures, combined with the appreciated hypervariability of their primary sequence, leads to a great diversity in the antigen combining site.

X-ray crystallographic studies demonstrate that the framework structures of the F_V of different antibodies assume a canonical structure regardless of the species of origin, amino acid sequence, or ligand specificity. This is generally taken as evidence that the ligand-binding characteristics of an antibody combining site are determined primarily by the structure and relative disposition of the CDRs, although some neighboring framework residues may also be involved in antigen-binding. Thus, if the fine specificity of an antibody is to be preserved, its CDR structures, and probably some of the neighboring residues, their interaction with each other and

with the rest of the variable domains, must also be maintained. These crystallographic studies point to the possible need for retaining most, if not all, of these residues.

While at first the necessity of retaining these amino acids might seem to prevent reaching the goal of decreasing immunogenicity by "humanization", the actual number of amino acids that must be retained is usually relatively small because of the striking similarity between, for example, human and murine variable regions.

Using either the buried-residue-retention technique ("BR-R"), or the buried-residue-modification technique ("BR-M"), humanization of the variable region of a non-human antibody, e.g., a murine antibody, begins with the identification of "important" xenogeneic amino acids to be retained. In both the BR-R technique and the BR-M technique, amino acid residues that are involved in antigen binding, or that contact the CDRs and/or an opposite chain of the antibody are assigned to the category of "important" residues to be left in their original form, e.g., in murine form.

The two methods differ strikingly, however, with respect to their treatment of buried amino acid residues, i.e. those having side-chains that are not exposed on the surface of the molecule. In particular, the BR-R technique was based in part on the following two propositions: (i) buried amino acid residues might not be expected to contribute substantially to the antibody's antigenicity (e.g., the HAMA response elicited by a murine monoclonal antibody); and (ii) varying such buried residues might disrupt the underlying structure of the antibody chain, thereby decreasing or destroying the original avidity for which it was selected. Accordingly, in the BR-R technique, these buried residues are not modified from their original form. Thus, for example, applying the BR-R technique to the humanization of a murine antibody, the buried residues would be left as they were in the original murine form. Then, among the exposed residues, those residues that make up the CDRs, and those framework residues that contact the CDRs and/or the other chain, would be retained. The other exposed residues would preferably be humanized.

The BR-M method involves making the opposite decision with respect to the buried residues. That is, rather than retaining buried residues in their original form

(e.g. in the murine form), they are preferably humanized by replacement with amino acids corresponding to those in a human consensus model. The BR-M method was employed herein in the production of preferred humanized antibodies derived from Mc3. Unexpectedly, this additional humanization (which should further reduce the possibility of a HAMA response in humans) did not disrupt the ability of the CDRs to bind to the cognate antigen. On the contrary, as illustrated below, humanized Mc3 antibodies produced by the BR-M method exhibited specific high avidity binding to BA-46 that was fully comparable to that of the original murine antibody.

While the buried residues have been regarded as unlikely to contribute to immunogenicity, the present inventors believe that such residues can indeed influence immunogenicity, although the manner in which they do so may be indirect. In particular, even if a residue is relatively inaccessible to solvent, it can nevertheless exert a "pushing" or "pulling" effect on nearby surface residues. In other words, while the buried residues do not contribute to the primary structure of the antibody surface, they may well affect its shape. Since that shape can in turn influence immunogenicity, the present inventors have undertaken the modification of buried residues in an effort to create a more "human" antibody. Using our BR-M technique, we have suceeded in achieving such humanization without sacrificing the avidity of the heterologous antibody.

The humanization of a particular residue is accomplished by modifying that residue to resemble a residue found at the corresponding location in a "human consensus model". The human consensus model is determined by comparison to a variety of human antibodies as illustrated below.

Important residues can be identified from a well characterized three-dimensional structure. However, when direct structural data are not available, it is possible using the present methodology to predict the location of important framework residues by analyzing other related antibody structures, especially those whose variable light and heavy regions belong to the same class. The classes of variable regions can be determined from their amino acid sequence.

A method by which these important amino acids are identified has been described for the case of the amino acids with buried side chains by Padlan, E.A.

(Padlan, E.A., "A Possible Procedure for Reducing the Immunogenicity of Antibody Variable Domains While Preserving Their Ligand-Binding Properties", Molecular Immunology, 28:489-494 (1991)). The variable region structures of several antibodies were compared using a computer program that determines the solvent accessibility of the framework residues as well as their contacts with the opposite domain as described by Padlan, E.A. (1991), supra. Examination of such fractional solvent accessibility reveals a very close similarity in the exposure patterns of the V_H and the V_L domains. Put in simple terms, regardless of the particular antibody in question, and of its amino acid sequence, the buried residues occupy similar relative positions in most antibodies.

A similar analysis can be done by computer modeling, to determine which amino acids contact the CDRs and which contact the opposite domain. At this point, the Fab structures that are currently in the Protein Data bank (Bernstein,F.C., et al., J. Mol. Biol. 112:535-542 (1977)) may be examined to determine which FRs are probably important in maintaining the structure of the combining site. Thus, after a close inspection of many high resolution three-dimensional structures of variable regions, the positions of all important framework amino acids, that is, those that contact the CDRs, and the opposite domain, may be tabulated. Keeping these amino acids, as well as those from the CDRs, and finally those FR amino acids that may be involved in ligand binding, should insure to a great extent the preservation of affinity. The precise identification of FR amino acids that are involved in ligand-binding cannot be generalized since it varies for different antibodies. Nevertheless, conservative decisions can be made to preserve the amino acids located in FR that have a high probability of contacting the antigen. Many of these residues are located adjacent to the CDRs and at the N-terminus of both chains, because the surfaces of these regions tend to be contiguous with the CDR surfaces.

As described herein, it is in fact possible to retain all of these important amino acids in their original (heterologous) form, e.g. as they were in a murine monoclonal antibody, and yet produce a humanized version thereof that substantially resembles a human antibody and is thus less likely to elicit a HAMA response.

All the amino acids that are determined to be not important by either the BR-R or BR-M method can be replaced by their corresponding human counterparts, preferably selected from a human consensus sequence as illustrated below.

Designing a Preferred Framework for Use in the Humanization of an Antibody

There are at least 11 Fab structures, 2 from human and 9 from murine antibodies, for which the atomic coordinates are known and available in the Protein Data Bank. These antibodies, listed in Figure 1, have been used to develop a "positional consensus" of important classes of framework residues, as described below.

In a first category, certain contacts between side chains in the variable domains of the 11 Fabs have been collected and presented in Figures 2 to 4. The numbers shown in parentheses after each residue correspond to the number of atomic contacts in which the residue is involved. Only contacts involving side chain atoms are presented; and atoms are designated as being in contact if they are within the sum of their van der Waals radii (Case and Karplus, J. Mol. Biol. 132:343-368, 1979) plus 0.5 angstroms. The numbering scheme throughout is that of Kabat et al. ("Sequences of Proteins of Immunological Interest", 5th Ed. US Dept. of Health and Human Service, NIH Publication No.91-3242 (1991)).

Figure 2 illustrates framework residues in the V_L domains that are believed to contact CDRs. Framework residues in the V_H domains that are believed to contact CDRs are listed in Figure 3. Framework residues that are believed to contact the opposite chain (which presumably maintain the quaternary structure of the variable domains) are listed in Figure 4.

In a second category, inward pointing and buried residues are examined. An inward-pointing residue is designated as buried if at least 50% of its side chain is inaccessible to solvent. Solvent accessibilities can be computed using the program of M.L. Connolly (J. Appl. Crystallogr. 16, 548-558) and routines developed by S. Sheriff et al. (Proc. Natl. Acad. Sci. USA 82:1104-1107), as described by Padlan (Proteins: Struct. Funct. Genet. 7:112-124, 1990); residue exposure is defined in the context of an isolated domain. The buried residues in the V_L domains, i.e.,

those which are located in the domain interior, are listed in Figure 5. The buried residues in the V_H domain are listed in Figure 6.

A "conservative" positional consensus (which we typically utilize) would regard a position as important even if only one or a few of the antibodies examined had important residues at that position. By way of illustration, it can be seen in Figure 6 that many of the positions of buried residues in V_H regions were conserved across most or all of the antibodies sampled. However, position 9 was occupied by a buried residue in only one case (a proline residue in antibody HyHEL-10). Under a somewhat less conservative approach, one could exclude such positions that were only rarely occupied by an important residue.

The positional consensus sequence of important residues will vary depending on whether the buried residues are regarded as "important" or not (i.e. whether one is using the BR-R technique or BR-M technique).

Applying this methodology, one obtains the following conservative positional consensus for humanization of a V_L region using the BR-R technique:

1-7, 11, 13, 19, 21-23, 35-38, 43-49, 58, 60-62, 66, 67, 69-71, 73, 75, 78, 82-88, 98, 100, 102, 104 and 106.

A corresponding BR-R positional consensus for a V_H region is as follows:

1, 2, 4, 6, 9, 12, 18, 20, 22, 24, 27-30, 36-40, 43-49, 66-69, 71, 73, 76, 78, 80, 82, 82c, 86, 88, 90-94, 103, 105, 107, 109 and 111.

For application of the BR-M technique, a conservative positional consensus for a V_L region is as follows:

1-5, 7, 22, 23, 35, 36, 38, 43-46, 48,49, 58, 60, 62, 66, 67, 69, 70, 71, 85, 87, 88, 98 and 100.

A corresponing BR-M positional consensus for a V_H region is as follows:

1, 2, 4, 24, 27-30, 36-40, 43-49, 66-69, 71, 73, 78, 80, 82, 86, 91-94, 103 and 105.

These positional consensus sequences can be used as convenient "templates" for predicting the occurrence of an important residue in an antibody to be humanized, as illustrated below. The positional consensus sequences apply only to framework residues. (In preferred embodiments, CDR residues are always considered important and are therefore preferably retained. It is possible, however,

to modify one or more of these CDR residues without substantially disrupting antigen binding.)

A search through the tables of immunoglobulin sequences (Kabat et al., "Sequences of Proteins of Immunological Interest", 5th Ed. US Dept. of Health and Human Service, NIH Publication No.91-3242 (1991)), shows that many human variable domain sequences are already quite similar to the antibodies used for generating the positional consensus sequences. (See Figure 7, in which the degree of sequence similarity for a number of sampled antibodies is shown in parentheses as "n/m" where "n" is the number of identities in "m" homologous positions).

In our preferred humanization method, illustrated below, we do not use any single human antibody as a framework model. Rather, we use a consensus sequence based on the framework residues most representative of a subclass of human antibodies. That is, the consensus sequence has a maximum number of amino acids in common with all human frameworks of the same subclass. This is important because the goal of humanization is to avoid an immunological response against the engineered recombinant peptide. In practice, the sequences of the xenogeneic variable chains are aligned with the consensus sequences from all variable region subclasses of the target species and then the number of differences between the consensus sequence and corresponding important residues in the xenogeneic sequence are scored. The human consensus sequence(s) that score(s) the lowest number of differences is (are) then chosen. In the humanization of the Mc3 antibody, as illustrated below, we used consensus sequences representative of the human V_KIV and V_HI subclasses for humanizing the light and heavy chain variable regions, respectively.

If, in a certain case, there are too many differences in the chosen framework (e.g., more than about 16), then the same alignment procedure using all tabulated human sequences may be repeated in order to find a specific human framework whose similarity with the xenogeneic sequence is maximized at the positions of the important amino acids. Thus, most preferably, the target species FR should be a consensus sequence representative of a human subclass; but next in preference would be a framework representing residues that are fairly commonly

observed in human antibodies (e.g. sequences found in several antibodies even if they are not a consensus); or, absent that, the framework of any human antibody.

Figures 8 and 9 further illustrate that many of the important FR amino acids occur at similar positions in different antibodies, and many of these are flanking the CDRs. Among these flanking positions are most of the framework residues that are involved in contacts with the opposite domain as shown in Figure 4, and many of those which are in contact with the CDRs as shown in Figures 2 and 3 above. Moreover, almost all of the framework residues that have been observed to participate in the binding to antigen (Amit, A.G., et al., Science 233:747-753 (1986); Sheriff, et al., P.N.A.S. (USA) 82:1104-1107 (1987); Padlan, E.A., et al. ,P.N.A.S. (USA) 86:5938-5942 (1989); Tulip, et al., Cold Spring Harbor Symp. Quant. Biol. 54:257-263 (1989); Bentley, et al., Nature (London) 348: 254-257 (1990)), are in these flanking regions.

Thus, in these preferred methods for "animalization" or "humanization", not just the CDRs are retained, but also some of the residues immediately adjacent to the CDRs. These methods provide a much better chance of retaining more of the ligand-binding properties of the original antibody and, at the same time, producing an antibody that is much less likely to elicit an immunogenic response in a heterologous species (such as a HAMA response in humans). The likelihood of retaining the antigen binding properties of the original antibody is even greater if the first few amino acids in the NH_2-termini of both chains are also retained, since some of them are found to be in contact with CDRs as shown in Figures 2 and 3.

Humanization Protocol

Designing a humanization protocol involves applying the foregoing principles on a residue-by-residue basis to an antibody to be humanized (i.e. the "xenogeneic" or "heterologous" antibody, frequently a murine antibody). The first step is to simply align the xenogeneic sequence with the human FR consensus sequence and identify all differences in framework residues. Obviously, if the human residue at a given position in the consensus is identical to the xenogeneic counterpart, then no "humanization" is required at that position.

The next step is to identify xenogeneic residues that differ from the human consensus but which are likely to be "important" residues. Using the buried-residue-retention technique (BR-R), "important" residues (i.e. those that are to be retained) include: (i) residues within a CDR; (ii) residues that are likely to contact a CDR; (iii) residues that are likely to contact the opposite antibody chain; and (iv) buried residues. Using the positional consensus sequences as templates to predict the position of important framework residues, one can readily identify a set of residues to be maintained.

Under the buried-residue-modification (or BR-M) technique, the positional consensus sequence is adjusted to reflect the removal of buried residues from the class of "important" framework residues. Suitable BR-M positional consensus sequences are described above.

We have successfully applied these methods to the humanization of a murine monoclonal antibody, Mc3, that is expected to be particularly useful in the detection and treatment of breast cancer. The methods can be readily applied to the transformation of other antibodies from a first species into a form that is likely to be less immunogenic when administered to a second species.

Once particular residues are selected for retention or modification, the actual construction of modified variable regions can be conveniently achieved using PCR amplification with primers that are custom tailored to produce the desired mutations, or by gene synthesis. In preferred embodiments, DNAs encoding the humanized variable regions (which retained certain "important" murine residues) were then joined to DNAs encoding portions of the human constant regions in a hybrid vector. After transfecting the vector into myeloma cells, the fusion polypeptides were expressed, yielding humanized versions of the Mc3 antibodies.

The humanization procedures described herein are designed to minimize potential losses in antigen binding affinity that might result from altering the antibody framework. To further minimize the likelihood of an immunological response to the humanized antibody, target human amino acid sequences were used that comprise the consensus sequences of all appropriate human variable regions. Nevertheless, neither the exemplified amino acid changes nor the exemplified human target sequences are the only choices encompassed by this invention. Thus,

many other individual amino acid changes and permutations thereof can be made without substantially disrupting the avidity of the resulting antibody. These can be particularly useful in providing an expanded repertoire of antibodies, such as Mc3 derivatives, that are likely to be quite helpful in the diagnosis and treatment of breast cancer. For example, now that we have successfully sequenced the variable regions of the Mc3 antibody, a variety of recombinant Mc3 peptides can be prepared in which conservative mutations (including substitutions, deletions and additions) can be made that are calculated to be unlikely to disrupt avidity, guided by the information provided herein as well as knowledge in the art. Preferably, the variants retain a level of avidity that is at least about 20% that of the starting antibody (e.g. the murine Mc3), more preferably at least about 40%, still more preferably at least about 60%, still more preferably at least about 80%, most preferably at least about 90%.

A convenient method for predicting the suitability of potential substitutions is performed by checking to see whether a particular amino acid has been incorporated into that position in known naturally-occurring antibodies. Appearance of the amino acid in that position in known human and/or murine antibodies, especially antibodies having similar frameworks, suggests that it is not incompatible with the architecture of the variable region. Thus, although the human consensus residue is the most preferred, other preferred substitutions can be selected from residues that have been observed at corresponding positions in other antibodies, especially those that have been observed in several closely-related antibodies. An illustration of such comparisons is described, for example, in International Publication WO94/11509, published May 26, 1994, by Couto et al. (see, e.g., Tables 10 and 11).

The recombinant peptides of the present invention can be provided as non-glycosylated peptides but they are preferably used in glycosylated form. When provided in glycosylated form, the recombinant peptide may be operatively linked to a glycosyl residue(s) provided by the eukaryotic cell where it is expressed, or it may be cloned and expressed in a prokaryotic cell as the naked polypeptide and the glycosyl residue(s) added thereafter, for example by means of glycosyl transferases as is known in the art. Examples of glycosyl residue(s) that may be added to the recombinant peptide of the invention are N-glycosylated and O-glycosylated

residues, among others. The glycosyl residues added to the naked recombinant peptide may have a molecular weight of about 20 to 50,000 daltons, and more preferably about 100 to 20,000 daltons or greater, depending on the size and molecular weight of the peptide to which they are attached. However, other types of polysaccharides and molecular weights may also be present. Glycosyl residues and other modifying groups can also be attached to the naked recombinant peptide of the invention by chemical means as is known in the art.

A single CDR is the smallest part of an antibody known to be capable of binding to an antigen. The sequences of the V_L and V_H CDRs of the Mc3 exemplary recombinant is shown below. Thus, small peptides that have the sequence of a single CDR can bind antigen and are, therefore, suitable for imaging tumors in vivo. A CDR attached to an effector agent may be synthesized chemically or recombinantly encoded in a DNA segment. Such small molecules have great tumor penetration and extremely rapid clearing properties when compared to larger antibody fragments. In some cases, it is more convenient to produce these small molecules by chemical synthesis, as is known in the art, rather than by fermentation. In many cases, these small peptides are completely non-immunogenic and an immune response, such as the HAMA response, is altogether avoided. Also preferred are 2 and 3 CDR units per chain operatively linked to one another by 1 to 10 or more amino acids and up to the entire inter-CDR segment length as positioned in the variable regions.

Heavy and light chain recombinant variable regions may be obtained individually or in V_H/V_L pairs, or attached to an effector agent such as a constant region(s) or portions thereof, a drug, an enzyme, a cytokine, a toxin, a whole antibody, or any other molecule or radioisotope. The fragments of the recombinant variable regions may be synthesized chemically as is known in the art or from the DNA segments encoding the non-human variable regions. This may be attained by PCR amplification of the DNA with primers synthesized to contain the desired mutation(s) as is known in the art. Similarly, the fragments encoding recombinant variable regions may be synthesized chemically or obtained by established cloning methods of restriction digestion, ligation, mutagenesis, and the like, as is known in the art.

It is possible to combine for example a chimeric light chain with a humanized heavy chain and vice versa. Preferably, however, both the heavy and the light chains are humanized.

There are advantages to using the different molecular variants of the recombinant peptide depending on the specific applications for which they are intended, some of which are listed below.

a) Smaller molecules penetrate target tissues more efficiently and are cleared from the body much more rapidly than larger molecules.

b) Single chain molecules can be manipulated and synthesized more efficiently that multiple chain molecules.

c) Many of these variants can be synthesized efficiently and inexpensively in bacteria, including the non-glycosylated recombinants.

d) Bi-functional or multifunctional molecules may carry effector agents, such as enzymes, cytokines, toxins, radioisotopes, drugs, and other molecules, to a target tissue.

e) Having a repertoire of variants can be especially useful in diagnostic/therapeutic settings in which particular derivative versions of a basic antibody structure can be more or less useful in a given individual or a given class of individuals, or over time of administration.

The recombinant peptides and hybrid peptides of this invention encompass CDRs and/or recombinant variable regions, antibody fragments such as Fab, Fab', $F(ab')_2$, and the like, see, e.g., O'Kennedy, R., and Roben, P. (O'Kennedy, R., and Roben, P., "Antibody Engineering: an Overview", Essays Biochem. (England) 26:59-75 (1991)). Variable regions can also be combined with constant regions, catalytic fragments, enzymes, hormones, and other molecules such as drugs and linkers, transmitters, and toxins, among others. Since the specificity and affinity of the antibody can effectively target it to a specific site containing its cognate antigen, such combinations can be especially effective tools for imaging, therapy, and diagnostics.

Single-Chain Antigen-Binding Polypeptides

A method for constructing single chain antigen-binding polypeptides has been described by Bird et al. (Bird, R.E., et al., Science 242:243-246 (1988); Bird, R.E., et al., Science 244:409 (1989)). Single Chain F_v (scF_v or sF_v) are single chain recombinant peptides containing both V_L and V_H with a linker such as a peptide connecting the two chains (V_L-linker-V_H). The engineering may be done at the DNA level, in which case knowledge of the sequence is required. These recombinant peptides have the conformational stability, folding, and ligand-binding affinity of single-chain variable region immunoglobulin fragments and may be expressed in E. coli. (Pantoliano, M.V., et al., Biochem. (US) 30:10117-25 (1991)). The peptide linker binding the two chains may be of variable length, for example, about 2 to 50 amino acid residues, and more preferably about 12 to 25 residues, and may be expressed in E. coli. (Pantoliano, M.V., et al. (1991), supra). A recombinant peptide such as an scF_v may be expressed and prepared from E. coli and used for tumor targeting. The clearance profiles for scF_v in some situations fragments are advantageous relative to those of normal antibodies, Fab, Fab' or $F(ab')_2$ fragments. (Colcher, D., et al., J. Natl. Cancer Inst. 82:1191-7 (1990)). Another type of recombinant peptide comprises a V_H-linker-V_L and may have about 230 to 260 amino acids. A synthetic gene using E. coli codons may be used for expression in E. coli. A leader peptide of about 20 amino acids, such that of Trp LE may be used to direct protein secretion into the periplasmic space or medium. If this leader peptide is not naturally cleaved, the sF_v recombinant peptide may be obtained by acid cleavage of the unique asp-pro peptide bond placed between the leader peptide and the sF_v-encoding region (Houston, J.S., et al., "Protein Engineering of Antibody Binding Sites: Recovery of Specific Activity in an Anti-Digoxin Single-Chain F_v Recombinant Produced in E. coli.", PNAS (USA) 85 (16):5879-83 (1988)). The construction, binding properties, metabolism and tumor targeting of the single-chain F_v recombinant peptides derived from monoclonal antibodies may be conducted as previously described (Milenic, D.E., et al., Cancer Res. (US) 51 (23 pt1):6363-71 (1991); Yokota, et al., "Rapid Tumor Penetration of a single-chain F_v and Comparison with Other Immunoglobulin Forms", Cancer Res. (US) 52(12):3402-8 (1992)). This type of recombinant peptide provides extremely

rapid tumor penetration and even distribution throughout tumor mass compared to IgG or Ig fragments Fab and $F(ab')_2$.

Bifunctional scF_v-Fxn or Fxn-scF_v

An example of this type of recombinant peptide is a V_L-linker-V_H with an effector agent such as a hormone, enzyme, cytokine, toxin, transmitter, and the like. These hybrid recombinant peptides may be prepared as described by McCarney et. al. (McCarney, J.E. et al., "Biosynthetic Antibody Binding Sites: Development of a Single-Chain F_v Model Based on Antidinitrophenol IgA Myeloma MOPC 315", J. Protein Chem. (US) 10 (6):669-83 (1991)). A bi-functional hybrid recombinant peptide containing an F_c-binding fragment B of staph protein A amino terminal to a single-chain recombinant F_v region of the present specificity is also encompassed and may be prepared as previously described. (Tai, M.S., et al., Biochem. 29 (35):8024-30 (1990)). In this example of a hybrid recombinant peptide of this invention is a Staph. A fragment B (anti F_c)) - scF_v polypeptide. The order is backward of normal cases. This FB-sF_v may be encoded in a single synthetic gene and expressed as peptide in E. coli. This recombinant peptide is a good example of a useful multifunctional targetable single-chain polypeptide. A hybrid recombinant peptide also comprising antibodies to a human carcinoma receptor and angiogenin is also part of this invention. Angiogenin is a human homologue of pancreatic RNAse. This is an $F(ab')_2$-like antibody-enzyme peptide effector. Another hybrid recombinant peptide comprising a V_H-CH1 heavy chain-RNAse may be expressed in a cell that secretes a chimeric light chain of the same antibody. A secreted antibody of similar structure was shown to cause the inhibition of growth and of protein synthesis of K562 cells that express the human transferrin receptor (Rybak, S.M., et al., "Humanization of Immunotoxins", PNAS 89:3165-3169 (1992)).

Bi-specific Antibodies

A monoclonal antibody or antibody fragment may be incorporated into a bi-specific recombinant peptide as described, for example, by Greenman et al.

(Greenman, J., et al., Mol. Immunol. (England) 28 (11):1243-54 (1991). In this example, a bi-specific $F(ab')_2$ was constructed, comprising two F(ab') joined by a thioether linkage. Bi-specific antibodies may also be obtained when two whole antibodies are attached. Another way to obtain bi-specific antibodies is by mixing chains from different antibodies or fragments thereof. In this manner the "left" branch of the bi-specific antibody has one function while the "right" branch has another.

Phage Display Libraries

The recombinant peptides in accordance with this invention may be screened with a filamentous phage system. This system may also be used for expressing any genes of antibodies or fragments thereof as well as for screening for mutagenized antibody variants as described by Marks et al. (Marks, J.D., et al., "Molecular Evolution of Proteins on Filamentous Phage. Mimicking the Strategy of the Immune System", J.Mol. Biol. (England) 267 (23):1607-10 (1992)). A library of V_H and V_L genes or recombinants thereof may be cloned and displayed on the surface of a phage. Antibody fragments binding specifically to several antigens may be isolated as reported by Marks (Marks, J.D., "By-Passing Immunization. Human Antibodies from V-gene Libraries Displayed on Phage", J. Mol. Biol. (England) 222 (3):581-97 (1991)).

Covalent Oligosaccharide Modifications

The present recombinant peptides alone or as hybrid peptides comprising antibodies and fragments thereof may be, e.g., covalently modified utilizing oxidized oligosaccharide moieties. The hybrid recombinant peptides may be modified at the oligosaccharide residue with either a peptide labeled with a radioisotope such as ^{125}I or with a chelate such as a diethylenetriaminepentaacetic acid chelate with ^{111}In. The use of oligosaccharides provides a more efficient localization to a target than that obtained with antibodies radiolabeled either at the amino acid chain lysines or tyrosines (Rodwell, J.D. et al., "Site-Specific Covalent Modification of Monoclonal Antibodies: In Vitro and In Vivo Evaluations", PNAS (USA) 83:2632-6 (1986)).

Fragments derived from the variable regions can be bound by a peptide or non-peptide linker such as is known in the art. Examples of peptide linkers are polylysines, leucine zippers, EGKSSGSGSEJKVD (SEQ ID NO:66), and (GGGGS)x3 (SEQ ID NO:67), and non-peptide polymers, among others.

Effector agents such as peptides and non-peptides may also be attached to the recombinant peptides of the invention. These include non-peptide polymers, monomers, atoms, etc., which are discussed below.

In another aspect, this invention provides a polypeptide that comprises at least recombinant peptide of the invention and at least one effector agent operatively linked to the peptide, combinations thereof and mixtures thereof. The effector agents that can utilized in this invention comprise peptides such as the constant regions of an antibody, cytokines, enzymes, toxins, non-peptide polymers, monomers, and atoms such as metals. The polypeptides of the invention encompass peptides linked by disulfide bonds, including peptide polymers produced and secreted by a cell which is expressing a peptide of the invention.

In one particularly preferred embodiment, the effector agent may comprise an atom such a radioisotope, an enzyme or a fluorescent label. These effector agents are suited for in vivo and in vitro assays because they permit the identification of complexes formed by the peptide of the invention. Radioisotopes are particularly preferred for in vivo imaging. Polypeptide labeling is known in the art (Greenwood, F.C., et al., Biochem. J. 89:114-123 (1963)). When a glycosylated polypeptide is utilized, the radiolabel may be attached to the glycosyl residue as is known in the art (Hay, G.W. et al, in Methods in Carbohydrate Chemistry, Vol 5:357, Whistler, R.L. Ed., Academic Press, NY and London (1965)). Effector agents comprising a monomer may be therapeutic, immunogenic or diagnostic agents, radioisotopes, DNA, or RNA monomers, chemical linkers, chemical chelators, transmitter molecules, combinations thereof, or combinations thereof with peptide and non-peptide polymers or copolymers and atoms. Examples of therapeutic agents are anti-neoplastic drugs such as vincristine, intercalation drugs, adriamycin, enzymes, toxins and hormones, among others. Examples of immunogenic agents are other vaccines against tumors such as r carcinomas or for others purposes. Examples of diagnostic agents are radioisotopes and enzymes,

among others. Examples of therapeutic, immunogenic and diagnostic agents are toxins, vaccines, and radioisotopes, among others. Examples of radioisotopes are ^{111}In, ^{35}S, ^{90}Y, ^{186}Re, ^{225}Ac, ^{125}I and ^{99m}Tc, among others. Examples of DNA and RNA monomers are A, T, U, G, C, among others. Examples of chemical linkers are dithiobis(succinimidyl)propionate and bis-(sulfosuccinimidyl)suberate, among others. Examples of transmitter molecules are cAMP and cGMP, among others. Examples of toxins are ricin A-chain and abrin A-chain, among others.

When the effector agent is a non-peptide polymer linked to the recombinant polypeptide of the invention, it may comprise an ester, ether, vinyl, amido, imido, alkylene, arylalkylene, cyanate, urethane, or isoprene polymers, DNA polymers, RNA polymers, copolymers thereof and copolymers thereof with peptide polymers or monomers, or have labeled atoms attached thereto. Examples of these are polyesters, polyethers, polyethyleneglycols, polyvinyls, polyamido and polyimido resins, polyethylenes, polytetrafluoroethylene, poly(ethylene)terephathalate, polypropylene, silicone rubber, isoprenes and copolymers thereof, copolymers of silicone and carbonated polylactic or polyglycolic acid or collagen, and the like. Particularly preferred are biodegradable and bioresorbable or bioabsorbable materials, which if detached from the polypeptide and left in the systemic circulation will not damage endogenous tissues. The effector agent being a peptide may comprise antibodies such as IgA, IgG, IgM, IgE or IgD, the constant region of antibodies of a species different from the variable region or fragments thereof, and the CDRs, variable regions, Fab, Fab', $F(ab')_2$ fragments of antibodies of the classes described above, hormones, enzymes, peptide transmitters and whole antibodies, combinations thereof, and combinations thereof with non-peptide polymers, copolymers, monomers and atoms such as radioisotopes. Examples of peptide transmitters and hormones suitable for use herein are insulin, growth hormone, FSH, LH, endorphins, and TNF, among others. Examples of enzymes are peroxidase, LDH, alkaline phosphatase and galactosidase, among others.

The polypeptides of the present invention can be provided as an anti-tumor composition along with a carrier or diluent, preferably a pharmaceutically-acceptable carrier or diluent. The anti-tumor recombinant peptide and the hybrid polymer provided herein may be present in the composition in an amount of about

0.001 to 99.99 wt%, more preferably about 0.01 to 20 wt%, and still more preferably about 1 to 5 wt%. However, other amounts are also suitable. Carriers generally, and pharmaceutically-acceptable carriers in particular are known in the art and need not be further described herein. The carrier may be provided in a separate sterile container or in admixture with the polypeptide. Typically, saline, aqueous alcoholic solutions, albumin-saline solutions, and propylene glycol solutions are suitable. However, others may also be utilized. When utilized for therapeutic purposes the proteic material must be of a purity suitable for human administration, and the composition may contain other ingredients as is known in the art. Examples of these are other anti-neoplastic drugs such as adriamycin and mitomycin, cytoxan, PALA and/or methotrexate, among others. However, other therapeutic drugs, carriers or diluents, immunological adjuvants and the like may be also be added. When the composition described above is utilized for in vivo imaging, it may comprise about 0.001 to 99.9 wt% recombinant peptide, and more preferably about 0.01 to 25 wt% recombinant peptide. Typically, when the composition is utilized for therapeutic purposes it may contain about 0.001 to 99.9 wt% recombinant peptide, and more preferably about 0.01 to 30 wt% recombinant peptide. When utilized for the ex vivo purging of neoplastic cells from bodily fluids such as spinal fluid, the composition may comprise about 0.0001 to 50wt%, and preferably about 0.01 to 20wt% recombinant peptide. When applied to the in vitro diagnosis of tumors such as carcinomas the composition of the invention may comprise about 0.001 to 35 wt% recombinant peptide, and more preferably about 0.01 to 10 wt% recombinant peptide. Other amounts, however, are also suitable.

For Mc3 antibodies, in particular, such products have special utility in the treatment of tumors of the breast. "Humanized" or "partially humanized" recombinant Mc3 peptides will thus be useful for the diagnosis and treatment of breast cancers in humans. The humanized Mc3 antibodies are expected to be particularly suitable for repeated administration to a subject and for long term therapy, such as in the case of metastases and/or the reoccurrence of tumors. Of all recombinants described and encompassed herein, the ones most suitable for in vivo applications are those that exhibit low or no binding to serum antigens and to normal cells, like Mc3. Suitable for in vitro or ex vivo uses are those that exhibit

good binding to tumor cell antigens such as the carcinoma cell antigen and weak or no binding to normal cells, like Mc3. Even though a patient may have in circulation an interfering amount of a molecule that can bind the recombinant peptide, the peptide may still be administered after removal of such serum molecule either by ex-vivo procedures or by administration of flush doses of the recombinant peptide, or peptide polymer of the invention.

A kit for the diagnosis of tumors such as carcinomas may comprise, for example, a composition comprising Mc3 variant polypeptides of the present invention, a solid support, immunoglobulins of a different species selectively binding the constant regions of the Mc3 variant antibody, protein G or protein A, and instructions for its use. This diagnostic kit may be utilized by covalently attaching the antigen or the recombinant peptide of the invention or a fusion protein thereof to the solid support by means of a linker as is known in the art. In a particularly preferred embodiment, the support is coated with a polypeptide such as methylated albumin as described in US Patent No. 4,572,901. When a biological sample is added to a well, the recombinant peptide or peptide polymer of the invention will bind any BA46 antigen, present in the biological sample. If a competitive assay is utilized, to the solid supported antigen or hybrid peptide thereof are added a known amount of the recombinant peptide and the sample. Thereafter, γ-globulin, protein G or protein A in labeled form may be added for detection. Monoclonal antibodies may be prepared as described by Kohler and Milstein (Kohler, G. and Milstein, C., "Continuous Culture of Fused Cell Secreting Antibody of Predefined Specificity", Nature 256:495-497 (1975)). Suitable for use in this invention are antibodies such as IgG, IgM, IgE, IgA, and IgD. Protein A, protein G and γ-globulin may be obtained commercially.

A diagnostic kit for detecting tumors such as carcinomas, and more particularly human carcinomas is provided herein that comprises an anti-BA46 composition comprising a recombinant peptide or peptide polymer and an effector agent comprising an enzyme, a radioisotope, a fluorescent label and/or a peptide comprising the constant region of an antibody of the species for which use it is intended, or fragments thereof capable of binding anti-constant region immunoglobulins, protein G or A, anti-tumor antibody, anti-constant region

immunoglobulins, protein G or protein A, a solid support having operatively linked thereto an antigen which specifically binds to the anti-BA46 recombinant peptide of the invention and the antibody, and instructions for its use. When the effector agent comprises a peptide, such as the constant region of an antibody of the target species, the solid support may have operatively linked thereto an antibody which specifically binds to a portion of a fusion protein other than the antigen of the invention. This permits the binding of the anti-tumor recombinant peptide to the antigen molecule now attached to the solid support. Any complex formed between the recombinant peptide of the invention and the supported tumor antigen will, thus, remain attached to the solid substrate. A competitive assay may then be conducted by addition to the solid supported antigen of a known amount of the BA46 antigen and the sample. The amount of antigen present in the sample may be obtained from a dilution curve by addition of anti-constant region immunoglobulins, protein G, protein A or other antibody binding molecules, e.g., labeled, to bind the hybrid recombinant peptide that is now attached to the support. This kit may be used in a competitive assay where the supported antigen molecule competes with antigen in the sample for a known amount of the recombinant peptide of the invention. The assay was described by Ceriani, R.L., et al. (Ceriani, R.L., et al., Anal. Biochem. 201:178-184 (1992)), the relevant text thereof being incorporated herein by reference.

A tumor such as a carcinoma may be imaged in vivo and/or diagnosed by administering to a subject suspected of carrying a carcinoma the anti-BA46 recombinant peptide or peptide polymer of the invention in radiolabeled form, in an amount effective to reach the tumor cells and bind thereto, and detecting any localized binding of the labeled recombinant peptide or peptide polymer to the tumor. Typically, the recombinant peptide or peptide polymer of the invention may be administered in an amount of about 0.001 to 5000 mg/kg weight per treatment, more preferably about 0.01 to 5000 μg/kg weight per treatment, and more preferably about 0.1 to 500 μg/kg weight per treatment. However, other amounts may also be utilized. Radiolabels that may be utilized are ^{111}In, ^{125}I, ^{99m}Tc, and ^{131}I, among others. These radioisotopes may be detected with various radioactivity

counting and imaging apparatuses known in the art, and in wide use by the medical community.

The presence of a tumor such as a carcinoma may also be diagnosed in vitro by contacting a biological sample with the anti-tumor recombinant peptide or peptide polymer of the invention to form an anti-tumor recombinant peptide-antigen complex with any tumor antigen present in the sample, and detecting any complex formed. The biological sample is typically obtained from a subject such as a human suspected of being afflicted with the tumor. Suitable biological samples are serum, blood, sputum, feces, lymph fluid, spinal fluid, lung secretions, and urine, among others, preferably blood or serum. Clearly, any source of fluid, tissue and the like may be prepared for use in this method as is known in the art.

In one preferred embodiment of the in vitro diagnostic method, the anti-carcinoma recombinant peptides or peptide polymers added to the biological sample comprises a labeled Mc3 variant polypeptide. Suitable labeling materials were described above. This method may be practiced, with the solid support containing kit described above, as a competitive assay as disclosed by Ceriani, R.L., et al. (supra).

The present recombinant peptides are also applicable to the purging of neoplastic cells, such as carcinoma cells, from biological samples, be it fluid or tissue samples. The purging of neoplastic cells from a fluid sample is part of the invention and may be practiced by contacting a biological fluid suspected of comprising neoplastic cells with the recombinant peptide of the invention, which is capable of selectively binding to an antigen of the neoplastic cells and allowing the peptide to bind to the antigen, and separating the recombinant peptide-cell complex from the remainder of the fluid.

This method may be utilized for purging unwanted cells ex vivo by extracting a biological sample from a patient, eliminating the neoplastic cells therefrom by separation of the recombinant peptide-cell complexes or by further addition of an effector such as complement or a toxin or a radioactive label that can act upon the cell and then replenishing the purged sample to the patient. This is typically suitable for use with spinal taps where spinal fluid is rid of neoplastic cells

such as carcinoma cells prior to reinjection. Other fluids may also be treated in this manner.

The present recombinant peptides or peptide polymers may also be applied to the histochemical assessment of the presence of neoplastic cells such as carcinoma cells in a tissue obtained from a subject suspected of being afflicted by a carcinoma by methods that are standard in the art, like the preparation of tissue slices and fixation on a solid substrate to permit the application of the peptide and then the assessment of any binding to neoplastic cells in the sample as indicated by the formation of complexes between the recombinant peptide and antigens on or in the cells.

The growth or the size of a primary or metastasized tumor or neoplasia such as a carcinoma may be inhibited or reduced by administering to a subject in a need of the treatment an effective amount of the anti-tumor recombinant peptides or peptide polymers of the invention. Typically, the recombinant peptides or peptide polymers may be administered in an amount of about 0.001 to 2000 μg/kg body weight per dose, and more preferably about 0.01 to 500 μg/kg body weight per dose. Repeated doses may be administered as prescribed by the treating physician. However, other amounts are also suitable. Generally, the administration of the recombinant peptide or peptide polymer is conducted by infusion so that the amount of radiolabel, toxin or other effector agent present that may produce a detrimental effect may be kept under control by varying the rate of administration. Typically, the infusion of one dose may last a few hours. However, also contemplated herein is the constant infusion of a dose for therapeutic purposes that will permit the maintenance of a constant level of the hybrid polypeptide in serum.

The infusion of the recombinant peptide or peptide polymer of the invention may be conducted as follows. Intravenous (i.v.) tubing may be pretreated, e.g., with 0.9% NaCl and 5% human serum albumin and placed for intravenous administration. The prescribed dose of the recombinant peptide or peptide polymer may be infused as follows. Optionally, unlabeled recombinant peptide or peptide polymer may be infused initially. 30 minutes after completion of the unlabeled infusion, ^{111}In-labeled and/or ^{90}Y labeled recombinant peptide or peptide polymer may be infused. The i.v. infusion may comprise a total volume of 250 ml of 0.9 %

NaCl and 5 % human serum albumin and be infused over a period of about 2 hours depending on any rate-dependent side effects observed. Vital signs should be taken every, e.g., 15 minutes during the infusion and every one hour post infusion until stable. A thorough cardiopulmonary physical examination may be done prior to, and at the conclusion, of the infusion. Medications including acetaminophen, diphenhydramine, epinephrine, and corticosteroids may be kept at hand for treatment of allergic reactions should they occur. The administration of the recombinant peptide or peptide polymer of the invention may be repeated as seen desirable by a practitioner. Typically, once a first dose has been administered and imaging indicates that there could be a reduction in the size of the tumor, whether primary or metastasized, repeated treatments may be administered every about 1 to 100, and more preferably about 2 to 60 days. These repeated treatments may be continued for a period of up to about 2 years, and in some circumstances even for longer periods of time or until complete disappearance of the tumor(s). The administration of the recombinant peptides or peptide polymers of this invention is typically more useful for therapeutic purposes when a primary tumor has, for example, been excised. Thus, it is preferably, for mopping up after surgical intervention or in cases of cancerous metastases that the present method is of most use. Also provided herein is a nucleotide sequence (DNA or RNA) encoding an Mc3 variant polypeptide; and vectors comprising DNA encoding Mc3, operably linked to a suitable promoter for expression of the polypeptides. Typically, vectors capable of replication both in eukaryotic and prokaryotic cells are suitable. When the preparation of a glycosylated recombinant polypeptide is desired the vector is preferably suitable for transfection of eukaryotic host cells.

This invention also encompasses a host cell that has been transfected with the hybrid vector described above. Suitable hosts are prokaryotic and eukaryotic hosts such as bacteria, yeast, and mammalian cells such as insect cells and non-producing hybridoma cells, among others. Suitable vectors and/or plasmids for the transfection of each one of these types of hosts are known in the art and need not be further described herein. Also known in the art are methods for cloning DNA sequences into each one of these types of vectors and for transfecting the different types of host cells.

The recombinant peptide which specifically binds to any antigen, may be produced by a method that comprises cloning the recombinant polydeoxyribonucleotide of the invention into a vector to form a hybrid vector, transfecting a host cell with the hybrid vector and allowing the expression of the recombinant peptide, and isolating the polypeptide or mixtures thereof. The DNA segment encoding the recombinant polypeptide may be obtained by chemical synthesis or by site-specific modification of the sequence encoding the variable region of the xenogeneic species by PCR amplification with specifically designed primers as is known in the art. The fragment DNAs may also be prepared by PCR with primers that introduce a stop codon at a desired position as is known in the art. The method may further comprise allowing the expressed recombinant peptides to interact with one another to form double chain recombinant peptides, one or both recombinant peptide chain comprising at least one xenogeneic CDR or variable region of the light or heavy chain of the antibody or fragment thereof modified as described above. Still part of this invention is a method of producing a hybrid recombinant peptide comprising an effector peptide and a humanized region which specifically binds to the antigen, the method comprising transfecting a host cell with the hybrid vector of this invention carrying a DNA sequence encoding the humanized region and the effector peptide, allowing the expression of the recombinant peptide, and isolating the recombinant peptide or mixtures thereof. The techniques for obtaining mRNA, conducting reverse transcription and PCR amplification of DNA, chemical synthesis of primers, cloning DNA sequences into a vector, transfecting a host cell, and purifying polypeptides from a culture medium are known in the art and need not be further described herein.

As an illustration of the methods described herein, the present inventors have undertaken the cloning, sequencing, and humanization of the murine monoclonal antibody Mc3 which is likely to be particularly useful in the diagnosis and treatment of human breast cancer.

Mc3 is a murine antibody that reacts with the human milk fat globule antigen BA46. We first constructed a chimeric version of Mc3 as described in Examples 1-

3 below. Next, we successfully humanized the variable regions of the Mc3 heavy and light chains using the BR-M technique as described herein.

The results described below confirmed that we could humanize Mc3 without sacrificing avidity. In particular, we detected no significant differences between the original and humanized forms of Mc3, as measured by their affinities (3×10^8 vs. 6.2×10^8 M^{-1}, respectively) and by their ability to compete for antigen binding. In a mouse model for human breast cancer, single doses of radiolabeled humanized Mc3 were found to distribute to the tumor site and help prevent the growth of the tumor.

The examples presented below are provided as a further guide to the practitioner of ordinary skill in the art, and are not to be construed as limiting the invention in any way.

EXAMPLES

Example 1: Cloning of cDNAs Encoding the V_L and V_H Chains of the Murine Monoclonal Antibody Mc3

The cDNAs encoding the variable regions of Mc3 were cloned, using the polymerase chain reaction (PCR). The utilized PCR primers were specific for the leader peptides and for the constant regions, respectively. Thus, the variable regions were contained in the PCR products but did not overlap with the primers. The PCR primers were purchased from Novagen (Madison, Wisconsin). Novagen manufactures primer collections specifically for cloning cDNAs encoding variable regions of murine cDNAs. The substrate for the PCR was polyadenylated RNA isolated from Mc3 hybridomas (Ceriani, R.L., *et al.* (1983) *Somatic Cell Genet* **9**(4): 415-27). The experimental details for cloning cDNAs encoding variable regions of antibodies, using PCR, have been previously described (Couto, J.R., *et al.* (1993) *Hybridoma* **12**(1): 15-23; and Couto, J.R., *et al.* (1993) *Hybridoma* **12**(4): 485-489).

In brief, the procedures utilized herein were for the reverse-transcription (RT) of RNAs encoding the variable regions and the subsequent amplification of the cDNAs by the polymerase chain reaction. The polyadenylated RNA was isolated with a FAST TRACK (TM) mRNA isolation kit (Invitrogen Corporation, San Diego, CA).

A PCR murine Ig primer set was purchased from Novagen (Madison, WI), and complementary DNA (cDNA) was prepared with an RNA PCR kit (Perkin Elmer-Cetus, Norwalk, CT).

Two different and degenerate "leader peptide" primers combined with a single degenerate "constant region" primer were utilized for each of the isolations, and in each case three independent isolations were performed. Thus, we isolated three independent cDNA clones encoding the variable region of the heavy chain (V_H), and another three independent clones encoding the variable region of the light chain (V_L). These PCR products were directly inserted into the TA cloning vector pCRII (Invitrogen). In each case both strands of the resulting inserts were sequenced. The sequences of the three V_H independent isolates were all identical

as were the sequences of the three independent V_L isolates. The V_H and V_L DNA sequences and their derived protein sequences are shown in Figures 10 and 11, respectively.

Nucleotide sequence of V_H-signal peptide region:

The following sequence encodes a functional signal peptide. This sequence, however, may not be the natural one since by using a PCR primer that is specific for the first part of the signal peptide, to clone the V_H cDNA, we lost the original sequence information for that region. Thus, the first 26 nucleotides of the following sequence may be different in the natural gene.

ATG AAA TGC AGC TGG GTC ATT CTC TTC CTC CTG TCA GGA ACT GCA GGT GTC CAC TCT (SEQ ID NO:68)

Derived protein sequence of V_H signal peptide:

The first 9 amino acids of the following sequence may not be identical to the original ones. See note for signal peptide-encoding DNA above.

M K C S W V I L F L L S G T A G V H S (SEQ ID NO:69)

Nucleotide sequence of V_L-signal peptide:

The following sequence encodes a functional signal peptide. This sequence, however, may not be the natural one since by using a PCR primer that is specific for the first part of the signal peptide, to clone the V_L cDNA, we lost the original sequence information for that region. Thus, the first 19 nucleotides of the following sequence may be different in the natural gene.

ATG GAG TTC CAG ACC CAG GTC TTT GTA TTC GTG TTT CTC TGG TTG TCT GGT GTT GAC GGA (SEQ ID NO:70)

Protein sequence of V_L signal peptide:

The first 7 amino acids of the following sequence may not be identical to the original ones. See note for signal peptide-encoding DNA above.

M E F Q T Q V F V F V F L W L S G V D G (SEQ ID NO:71)

Complete sequence of V_H and V_L

The complete nucleotide and amino acid sequence for the variable region of the heavy chain of Mc3 is shown in Figure 10. The complete nucleotide and amino acid sequence for the variable region of the light chain (kappa) of Mc3 is shown in Figure 11. The identification of the sequences was done by comparing them with the databases published by Kabat et al, supra. Amino acids are shown in the one letter code. Lower case amino acids represent the leader peptides. Lower case nucleotides represent primer sequence overlaps and may, therefore, not correspond to the natural sequences.

Example 2: Construction of ChMc3 Genes, Chimeric Version of Mc3 with Human Constant Regions

DNA fragments encoding the V_H and V_L regions as well as appropriate leader peptides were amplified, by PCR, directly from the respective pCRII clones described above, using primers that contained appropriate terminal restriction sites for insertion into expression vectors. The PCR primers used for this purpose were as follows:

Primer name: JO65

Terminal Restriction site: SalI

Primer specificity: Kappa chain, J region

Primer direction: antisense.

Primer sequence:

GTCGACTTAC G TTT TAT TTC CAA GTT TGT CCC CGA GCC

(SEQ ID NO:72)

Primer name: JO66

Terminal Restriction site: NheI

Primer specificity: Heavy chain, J region

Primer direction: antisense.

Primer sequence:

GCT AGC TGA GGA GAC GGT GAC TGA GGT TC (SEQ ID NO:73)

Primer name: JO67

Terminal Restriction site: EcoRV

Primer specificity: Kappa chain, signal peptide

Primer direction: sense

Primer sequence:

GATATC CACC ATG GAG TTC CAG ACC CAG GTC TTT GTA TT

(SEQ ID NO:74)

Primer name: JO68

Terminal Restriction site: HpaI

Primer specificity: Heavy chain signal peptide

Primer direction:sense

Primer sequence:

GTTAAC CACC ATG AAA TGC AGC TGG GTC ATT CTC TT

(SEQ ID NO:75)

Vent DNA polymerase (New England Biolabs) was used in these PCRs because of its high fidelity. Reaction conditions were as described in the New England Biolabs catalog. The resulting V_H and V_L-encoding PCR products were inserted first into pBLUESCRIPT II (TM) (Stratagene) that had been digested with EcoRV. The resulting intermediate clones were then digested with the appropriate restriction enzymes, see above, and the DNA inserts were transferred into vectors pAH4604 and pAG4622 respectively.

These vectors, which, encode either a human gamma 1 constant region or a human kappa constant region, were developed (Coloma, M.J., *et al.* (1992) *J Immunol Methods* **152**(1): 89-104) and kindly provided by S.L. Morrison (Dept. of Microbiology and Molecular Genetics, UCLA). The inserts were again sequenced in both directions directly in the pAH4604 and pAG4622 vectors. Both vectors were derived from pSV2 (Mulligan, R.C., and Berg, P. (1980) *Science* **209**:1422-1427), and contain genomic fragments encoding either the heavy or the light chain constant domains. The vectors accept cDNAs that encode the F_v regions. To ligate the F_v cDNAs to the vectors, restriction ends were added to the cDNAs in a set of PCR reactions, using the JO65, JO66, JO67 and JO68 primers.

The pAG4622 light chain vector contains the gene for the human κ chain constant region, including the J-C intron. It encodes xanthine-guanine phosphoribosyl-transferase or gpt (Mulligan, R.C., and Berg, P.(1981) *PNAS (USA)* **78**:2072-2076) as a dominant selectable marker. It accepts the murine V_L cDNA between the ribosome binding site (Kozak, M. (1984) *Nucleic Acids Res.* **12**:857-872), which is preceded by the V_H promoter from the anti-dansyl murine monoclonal antibody 27.44 (Coloma, M.J., *et al.* (1992) *J Immunol Methods* **152**(1): 89-104), and the J-C intron. The J-C intron contains the k chain enhancer (Potter, H., et al. (1984) *PNAS (USA)* **81**:7161-7165; and Emorine, L., et al.(1983) *Nature* **304**: 447-449).

The pAH4604 heavy chain vector contains the gene for the heavy chain γ1 constant region, but no J-C intron. It encodes histidinol-dehydrogenase or hisD (Hartman, S.C. and Mulligan, R.C. (1988) *PNAS (USA)* **85**:8047-8051) as a dominant selectable marker. It accepts the murine V_H cDNA between the dansyl promoter-ribosome binding site and the constant γ1 gene. The vector also contains an insert that encodes the heavy chain enhancer (Rabbitts, T.H., et al (1983) *Nature* **306**: 806-809).

Example 3: Preparation and Characterization of Chimeric Mc3 (ChMc3) Antibodies

All the procedures utilized in this Example have been described in detail in previous publications (Couto, J.R., *et al.* (1993) *Hybridoma* **12**(1): 15-23; and Couto, J.R., *et al.* (1993) *Hybridoma* **12**(4): 485-489). Tissue culture conditions were generally as follows: SP2/0-Ag14 cells (Shulman, M., et al. (1978), below) were cultured either in Dulbecco's modified Eagle's medium (DME): fetal bovine serum (FBS), 90:10 (v/v) or in a mixture of DME:RPMI:FBS, 45:45:10 (v/v/v) or RPMI:FBS, 90:10 (v/v). Penicillin and streptomycin were added to prevent bacterial growth. When serum-free medium was utilized, it contained an HL-1 supplement as directed by the manufacturer (Ventrex Labs., Portland, ME). The freezing medium was 10% DMSO in bovine serum.

In brief, after sequence verification, both plasmid constructs were electroporated into SP2/0-Ag14 myeloma cells. Supernatants from stable transfectants were assayed for the presence of the chimeric antibody. The secreted

chimeric antibody was first captured by plate-bound goat anti-human kappa chain polyclonal antibody, and subsequently developed with a radiolabeled secondary goat anti-human gamma chain polyclonal antibody. The chimeric antibody was also assayed for binding to a plate-bound human milk fat globule (HMFG) preparation.

Stable transfectants expressing chimeric antibody that bound to HMFG were first cloned and then cultured in serum-free protein-free medium (Sigma cat.# S2772). ChMc3 was then purified from the medium using a protein A column (BioRad). The purified antibody ran as a single wide band on 7.6 % non-reducing SDSPAGE. Its migration on the gel matched that of other purified antibodies loaded on the same gel. Under reducing conditions this band resolved into two bands of approximately 53 kDa and 29 kDa respectively, and their migration matched those of other reduced antibodies loaded on the same gel.

Example 4: Determination of the Affinity of ChMc3 for HMFG

The antibody-antigen affinity constants for the murine-human chimeric (ChMc3) antibody were determined by obtaining the reciprocal value of the concentration of competing unlabeled monoclonal antibody giving 50% binding as described by Sheldon et al. (1987) *Biochem. Cell Biol.* **65**: 423-428. The protocol for the assay was as follows.

Microtiter plates (Dynatech, Chantilly, VA) were prepared with HMFG according to standard techniques (as described by Ceriani et al., in "Monoclonal Antibodies and Functional Cell Lines" (T.J. McKern et al. eds.), pp. 398-402, New York, Plenum Press, 1984). To each well was added 25μl ^{125}I-Mc3 in RIA buffer (10% bovine calf serum, 0.3% TRITON (TM) X-100, 0.05% sodium azide pH 7.4, in phosphate buffered saline), and competed with 25 μl of either unlabeled murine antibody or murine-human chimeric antibody in RIA buffer at final concentrations in the nanomolar range.

Iodinations were performed with ^{125}I (17 Ci/mg, Nordion International Inc., Kanata, Ontario, Canada). 50 μg monoclonal antibody Mc3 was labeled (at a specific activity of ~10 mCi/mg) using the chloramine T method as described by Ceriani, R.L., and Blank, E.W. (1988) *Cancer Res.* **48**: 4664-4672. When the cpm of bound radiolabeled murine Mc3 (MuMc3) antibody was plotted on the Y

axis and the logarithm of the nanomolar (nM) concentration of competing unlabeled MuMc3 antibody or murine human chimeric (ChMc3) antibody was plotted on the X axis, the antibodies exhibited similar competition profiles (Figure not shown).

The affinity of the purified Chimeric antibody (ChMc3) for HMFG was determined to be $5 \times 10^8\ M^{-1}$, which closely matches the observed affinity constant for the Mc3 murine antibody of $3 \times 10^8\ M^{-1}$. Furthermore, we determined in competition experiments that ChMc3 competes as well as Mc3 against the binding of radiolabeled Mc3 to HMFG. Thus, both the affinity and the specificity of the original murine antibody were preserved in its chimeric counterpart. These affinity and competition results further indicate that the antibodies are authentic.

Example 5: Identification of a Human Consensus Model for Directing the Humanization of Mc3

We reasoned that the least immunogenic humanized version of Mc3 would be one in which the V_L and V_H sequences approximated the consensus sequences of human V_L and V_H subclasses, respectively. Thus, rather than choosing the V_L and V_H sequences of a particular antibody as targets, we chose the consensus sequences of the human V_KIV and V_HI subclasses, for V_L and V_H respectively (Kabat, E. A. *et al.* (1991). Sequences of proteins of immunological interest. U.S. Dept. Health and Human Services, NIH).

These human consensus variable regions are the most similar to the corresponding variable regions of Mc3. Most of the important framework residues were identical in the murine and in the human consensus frameworks, but some were not. The human consensus model for the variable region of the heavy chain of Mc3 is shown in Figure 12 and that for the light chain variable region is shown in Figure 13.

Positions in which the murine residue differed from the human consensus residue were then analyzed according to either the BR-R technique or the BR-M technique, to determine whether the residue should or should not be modified for humanization, as illustrated below.

Example 6: Application of the Buried-Residue-Modification (BR-M) Technique to the Humanization of Mc3

Using the buried-residue-modification technique (or BR-M technique), "important" residues that are to be retained include: (i) residues within a CDR; (ii) residues that are likely to contact a CDR; (iii) residues that are likely to contact the opposite antibody chain. In contrast to the BR-R technique, the buried residues can be, and preferably are, humanized.

The probable sequence position of the "important" residues, was determined by applying a conservative positional consensus developed for application of the BR-M technique, as described above. The positional consensus for V_L was as follows: 1-5, 7, 22, 23, 35, 36, 38, 43-46, 48,49, 58, 60, 62, 66, 67, 69, 70, 71, 85, 87, 88, 98, and 100. For V_H, it was as follows: 1, 2, 4, 24, 27-30, 36-40, 43-49, 66-69, 71, 73, 78, 80, 82, 86, 91-94, 103, and 105.

The application of the BR-M method to the humanization of the Mc3 variable regions is illustrated on a residue-by-residue basis in Figure 12 and Figure 13, for the heavy and light chains of Mc3, respectively.

The BR-M humanization protocol can be summarized as follows (using the terms shown in Figure 12 and Figure 13):

Under the heading "**Murine retained**":

Yes (same as human)	murine residue identical to human consensus, humanization not required
Yes (CDR)	murine residue differed from human consensus but residue appeared to be within CDR, murine retained
Yes (contact CDR)	murine residue differed from human consensus but residue likely to contact CDR, murine retained

Yes (interchain cont.)	murine residue differed from human consensus but residue likely to contact opposite chain, murine retained
No	residue did not fit any of the preceding categories and was humanized (by substituting human consensus residue)

Under the heading "**Humanized**":

n/a	murine residue identical to human consensus, humanization not required
Humanized	humanized residues if they were not "important" murine residues (as described above)
Humanized (BR)	indicates that the humanized residue was likely to be a buried residue (such a residue would have been retained under the BR-R technique)
Not humanized	retained a murine residue that was considered "important"

As shown in Figure 13, the final humanized version of V_K differs only at three FR positions from the corresponding V_KIV human consensus sequence (Kabat, E. A. *et al.* (1991). Sequences of proteins of immunological interest. U.S. Dept. Health and Human Services, NIH). The differences between the humanized heavy chain and the human consensus for V_HI are more numerous, 13 FR positions. Nevertheless, a considerable fraction of human antibodies belonging to

this subfamily contain more differences in FR positions from their own consensus sequences than HuMc3 V_H does. Thus, for example, we found certain human V_HI frameworks with as many as 29 differences from their own consensus sequences. The number of buried framework residues that were changed from murine to human were 7 in V_K and 5 in V_H.

Example 7: Application of the Buried-Residue-Retention (BR-R) Technique to the Humanization of Mc3

Using the buried-residue-retention technique, all murine residues that are likely to be buried are retained.

In order to apply the BR-R technique to the humanization of Mc3, all of the residues labelled "Humanized (BR)" in Figures 12 and 13 would have been left in their original murine form. Other aspects of the humanization protocol would be identical.

The amino acid sequence of a BR-R humanized form of the Mc3 variable heavy region is shown in Figure 14 (using the standard one-letter amino acid code; lower-case letters indicate leader peptide). The corresponding sequence for the Mc3 light chain is shown in Figure 15.

Example 8: Construction of HuMc3 Genes, Humanized Versions of the Chimeric Mc3 Genes

The entire regions to be humanized were synthesized by the overlapping oligonucleotide PCR method (Ye, Q. Z. *et al.* (1992) *Biochem Biophys Res Commun* **186**(1): 143-9). Oligonucleotides varying in size from 49 to 101 nucleotides, were synthesized on a PCR-Mate EP DNA synthesizer model 391 (Applied Biosystems, Foster City CA.) using 40nmole columns, cycle 1:63, with Trityl off. The oligonucleotides were not purified prior to their use and their concentrations were estimated using the formula $c=[(A_{260})/30]\mu g/\mu l$.

Primers used in the construction of HuMc3 genes are shown in Figures 16 and 17. PCR conditions were as follows: 150nM each of four long (100-101'mers) internal oligonucleotides, 2μM each of two short (49-66'mers) terminal primers, 200μM each dNTP, 10mM KCl, 20mM Tris-HCl pH 8.8, 10mM $(NH_4)_2SO_4$,

0.1% TRITON (TM) X-100, 6mM $MgSO_4$. Vent DNA polymerase (New England Biolabs), 2 units per 100μl reaction was added after File 2, below, (hot start). A GENEAMP (TM) PCR system 9600 (Perkin Elmer Cetus) was programmed with the following series of linked files: File 1=[(95°, 5 min), (1 min ramp to 70°), (5 min pause)]; File 2=[(96°, 5 sec) (55°, 10 sec) (72°, 30 sec)]x3; File 3=[(96°, 5 sec) (60°, 10 sec) (72°, 30 sec)]x29; File 4=[(72°, 10 minutes)]; File 5=[(5°, forever)]. File 4 was repeated at the end of the PCR, after adding extra dNTPs (to 120μM each) and 1 unit of Vent DNA polymerase (per 100μl reaction).

The synthetic DNA fragments were first inserted into EcoRV-digested pBLUESCRIPT II (TM) (Stratagene). Once the sequences of the synthetic DNA cassettes were confirmed in the small intermediate plasmids, appropriate restriction fragments were then transferred into the expression plasmids. V_H, encoded in an EcoRV-NheI fragment was inserted into pAH4604 and V_K, encoded in an EcoRV-SalI fragment was inserted into pAG4622 (Coloma, M. J. *et al.* (1992) *J Immunol Methods* **152**(1): 89-104; Couto, J. R. *et al.* (1993) *Hybridoma* **12**(1): 15-23; and Couto, J. R. *et al.* (1993). *Hybridoma* **12**(4): 485-489).

The nucleotide and corresponding polypeptide sequences of the humanized V_H region of HuMc3v2 are shown in Figure 18. The nucleotide and corresponding polypeptide sequences of the humanized V_L region of HuMc3v2 are shown in Figure 19.

Example 9: Preparation of Humanized Mc3 (HuMc3) Antibody

The humanized variable regions from Example 5 (HuMc3) were cloned into the expression vectors pAG4622 and pAH4604. As described in Example 2 above, these vectors were used to express the resulting recombinant antibody. The construction and expression of the humanized antibody genes were performed as described for the chimeric antibody in Example 3 (as well as Couto, J. R. *et al.* (1993) *Hybridoma* **12**(1): 15-23; and Couto, J. R. *et al.* (1993). *Hybridoma* **12**(4): 485-489). The non-producer myeloma cell line SP2/0-Ag14, ATCC:CRL 1581 was transfected, and antibody-producing clones were isolated as described in Example 3 and in Couto, J. R. *et al.* (1993) *Hybridoma* **12**(1): 15-23; and Couto, J. R. *et al.* (1993). *Hybridoma* **12**(4): 485-489. Antibody production was boosted by the

standard method of adding OPTIMAB (TM) (Gibco catalog 680-191 OSD) to the culture medium at a concentration of 1% of each of the components A and B.

Colonies that secreted the highest levels of antibody into the supernatants were subcloned into serum-free protein-free medium. Antibody levels in the medium were measured by standard radioimmunodetection techniques (Couto J.R. et al. (1993), Hybridoma 12:15-23). A plate-bound goat anti-human-κ capturing antibody was used with a ^{125}I-labeled goat anti-human-κ secondary antibody, and the values obtained were compared with those from a standard dilution curve obtained in parallel using an unrelated human $IgG_1\kappa$ immunoglobulin (Sigma catalog I-3889).

Antibody was purified from the culture supernatant of Sp2/0-Ag14 transfectants by a method similar to that of Example 3: The secreted monoclonal antibodies were concentrated through an Amicon DIAFF (TM) YM30 ultrafiltration membrane and purified using a protein A column (Ceriani et al. (1992), Anal Biochem 201:178-184). Purity was verified by SDS-PAGE. Purified HuMc3 ran as a single wide band on 7.6% non-reducing SDS-PAGE. Under reducing conditions, two bands were observed with apparent molecular weights of approximately 53 kDa and 29 kDa.

Example 10: Functional comparison of HuMc3 and MuMc3

The affinity of HuMc3 for HMFG was measured similar to the method described in Example 3, to confirm that it had comparable binding activity to the mouse and chimera antibodies from which it had been derived.

MuMc3, HuMc3, and a human $IgG_1\kappa$ of unrelated specificity were radiolabeled as in Example 4. Specific activities obtained were between 6 and 20 mCi/mg.

Binding studies were conducted as outlined earlier. Briefly, microliter plates were prepared using successive layers of methylated BSA (bovine serum albumin), glutaraldehyde, and a preparation of delipidated HMFG (Ceriani R.L. et al. (1977) PNAS (USA) 74:582-586). Each well was coated with 100 ng of HMFG. Competition experiments were conducted by adding to each well a standard amount

of ^{125}I-MuMc3 and an appropriate dilution of unlabeled MuMc3 or HuMc3 in RIA buffer (10% bovine calf serum, 0.3 TRITON X-100 (TM), 0.05% sodium azide pH 7.4, in PBS). For the determination of affinity constants, each antibody was tested in competition against itself. The affinity constant was calculated as the reciprocal of the concentration of competing unlabeled monoclonal antibody that gave 50% maximal binding.

The observed affinities of the MuMc3 and HuMc3 for a preparation of human milk fat globule were respectively 3 x 10^8 M^{-1} and 6 x 10^8 M^{-1}. These numbers confirm that the recombinant antibodies retain binding activity for HMFG, and that the humanization procedure did not substantially alter the affinity of the original antibody.

Differences in the epitopes recognized by two related antibodies can be detected when both compete for binding to their common antigen. Figure 20 shows results obtained when radiolabeled MuMc3 was used in competition experiments against either unlabeled MuMc3 (open circles) or unlabeled HuMc3 (filled circles). Values on the Y-axis represent the amount of ^{125}I-MuMc3 bound in the presence of competing unlabeled antibody, relative to the binding in the absence of competing antibody. The results show that MuMc3 and HuMc3 compete equally well against labeled MuMc3, indicating that they bind to identical or closely related epitopes.

Example 11: Biodistribution studies

HMFG antigen is known to be associated with human breast cell cancers, and has been used as a target for antibody-mediated detection and therapy. As described earlier, HuMc3 was designed to be a useful targeting agent to carry pharmacological effectors, such as radioisotopes, to tumor sites. In this Example, radioiodinated HuMc3 antibody and the MuMc3 control were used in biodistribution studies in a mouse model of human breast carcinoma to confirm that the binding activity demonstrated in the microtiter plate assays was also observable in vivo.

Athymic nu/nu mice, 11 to 12 weeks old, were purchased from Simonsen (Gilroy, CA). They were maintained in sterilized caging and bedding, and fed

irradiation-sterilized Purina mouse chow 5058 and sterilized tap water acidified to pH 2.5. The mice were kept at a temperature of 25.6°C to 28.9°C on a cycle of 12 h light and 12 h dark.

The transplantable human mammary tumor MX-1 was obtained from the EG&G Mason Research Institute (Worcester, MA) (Inoue K. et al. (1983) Chemother Pharmacol 10:182-186). The tumor was established in nu/nu mice at our facility according to standard protocols. Tumors were grown for 22 days, and experimental radioimmunotherapy was begun on mice whose mean tumor volume was approximately 100 mm^3. Tumor volumes were measured with a caliper, and calculated by multiplying the length x width x height of the tumor mass and dividing by 2. Tumors were ranked according to tumor volume, and the mice were grouped so that each group had approximately the same mean tumor volume.

MuMc3, HuMc3, and a human $IgG_1\kappa$ control antibody (Sigma 1-3889) were labeled with ^{131}I as described in Examples 4 and 10, except that $Na^{131}I$ was used in place of $Na^{125}I$. The specific activities were 12.15 mCi/mg, 9.0 mCi/mg, and 11.2 mCi/mg, respectively. Mice were injected with 10 μCi of labeled antibody as a single bolus. The tissues were dissected, weighed, and counted at various times after injection, and the percent of injected dose/gram of tissue was calculated, taking into account radioisotopic decay.

Figure 21 shows the results of the biodistribution studies. The four bars for each tissue site show the activity present after 1, 2, 4, and 8 days, respectively (mean $\pm$ standard error for 5 animals sacrificed at each time point). ^{131}I-labeled MuMc3 and HuMc3 antibodies persisted in the tumor increased over a period of at least 4 days (middle and lower panels). In all other tissues, bound antibody decreased steadily over this period. In comparison, the amount of ^{131}I-labeled non-specific antibody that localized to the tumor site was much smaller (upper panel).

Thus, HuMc3 showed the same tumor specificity as MuMc3. At 4 days after injection, the percent of injected HuMc3 at the tumor site was 21.3%, and at 8 days was 11.1%. Relative specific activity in the tissues was 2.5:1 (tumor:lung) and 25:1 (tumor:muscle) at 4 days. The relative specific activity was higher 8 days after injection.

Example 12: HuMc3 as a targeting agent for radiotherapy of breast cancer

Since the HuMc3 antibody binds and homes effectively to the BA46 antigen, it is a suitable carrier to convey a therapeutic dose of radioactivity to a tumor site. This was demonstrated directly in the murine MX-1 tumor model of Example 11, using a larger dose of radioactivity.

^{131}I was a useful radioisotope for this purpose for two obvious reasons: it is easy to work with for experimental purposes, and it has the properties that are known to be suitable for radioimmunotherapy. In particular, it emits particles with higher energy than ^{125}I and ^{99m}Tc and is therefore capable of providing a greater radiation dose per mCi; furthermore, the radiation is partly in the form of beta particles, which is readily absorbed by nearby tissues. Other radioisotopes frequently used for radioimmunotherapy include ^{111}In and ^{90}Y.

Thus, HuMc3 antibody was radiolabeled with ^{131}I as in Example 11, to a specific activity of 9.0 mCi/mg. MX-1 bearing nu/nu mice were prepared as before. Five MX-1 tumor-bearing athymic nu/nu mice were given a single i.p. injection of 500 μCi of ^{131}I-HuMc3, diluted in PBS (phosphate buffered saline) containing 0.1% BSA. Tumor volumes were followed for 30 days after injection, using the caliper method outlined in the previous Example. Six mice served as a control group, and were not injected with labeled antibody.

As shown in Figure 22, the initial tumor size for both treated and untreated groups was approximately 100 mm^3. In the treated mice, the average tumor size decreased to 42mm^3 at day 30 (lower line). In contrast, tumors in the uninjected group grew continuously to reach a final average size of 2,100 mm^3 (upper line). No deaths occurred in either of the groups in the first 30-days after therapy. At 61 days, all five treated animals were still alive, and one animal had no detectable tumor. These results suggest that HuMc3 is more effective in experimental radioimmunotherapy than monoclonal antibodies specific for other BA46 epitopes (Peterson et al. (1994) 353:1-8 in Antigen and Antibody Molecular Engineering in Breast Cancer Diagnosis and Treatment, Plenum Press NY).

Example 13: Efficacy of HuMc3 radiolabeled using a chelating agent

Still further experiments were conducted to demonstrate the suitability of humanized Mc3 as a targeting agent for radiotherapy.

As is known to a practitioner of ordinary skill in the art, when the antibody is to be used in a clinical setting or with an isotope that has a short half life, it is generally preferable to provide the antibody pre-conjugated to a linking group, which in turn is capable of receiving the radioisotope shortly before use. Preferred examples of such linking groups are chelators. See, generally, Brechbiel, MW et al. (1991), Bioconjugate Chem 2:187-194. An example of a preferred chelator linking group is MXDTPA. The chelator can be provided in purified form and conjugated to the antibody using buffers that are essentially free of metal ions. The conjugate is generally stored in a metal-free environment to avoid occupying the binding site in the chelator. Just before use, the conjugate can be mixed with a suitable radioisotope, such as ^{111}In or ^{90}Y, under conditions and at a molar ratio that permit essentially all the radioisotope to be captured and retained tightly by the conjugate.

Experiments were conducted to confirm that HuMc3 could be labeled with a chelator without perturbing the binding activity for HMFG, as observed in the previous Examples.

MXDTPA was obtained from O. Gansow at the NIH, Bethesda, MD. MXDTPA was conjugated to antibody according to standard protocols (Brechbiel MW et al. (1986), Inorg. Chem. 25:2272-2281), as follows: About 3-5 mg recombinant antibody or human $IgG_1\kappa$ control antibody were prepared by dialyzing overnight at 4°C against 1 liter of 0.15 M NaCl and 0.05 M Hepes buffer, pH 8.6. The MXDTPA was dissolved in metal-free water in a volume of 50 μL for each 5 mg. The conjugation was carried out by combining the antibody with the MXDTPA solution, and incubating for 19 h at room temperature. Free MXDTPA was removed from the conjugated antibody by dialysis against 3 changes of ammonium acetate buffer, pH 6.8, for 24 h each.

Pharmaceutical grade ^{111}In was obtained from Amersham, Arlington Heights, IL. Labeling was performed by adding the ^{111}In to the conjugated antibody as previously described (Blank EW et al. (1992) Cancer J 5:38-44).

Specific activities were 6 mCi/mg and 1.7 mCi/mg for the MuMc3 and HuMc3, respectively.

The integrity of ^{111}In-labeled antibody was determined by high-pressure liquid chromatography (HPLC). Perkin Elmer model 250 HPLC pump was used with a 600 x 7.5 mm TSK 250 gel filtration column. 0.1 mL samples comprising 1 x 10^5 cpm were run in a buffer of 0.15 M NaCl and 30 mM phosphate, pH 6.5 at 0.5 ml/min and a pressure of 70 bar. Fractions of 0.5 mL were collected and counted. Essentially all of the radioactivity eluted at a position corresponding to that of an IgG_1 standard.

Biodistribution studies were conducted using ^{111}In labeled antibody in the MX-1 human breast tumor mouse model, as in Example 11. Each mouse received a single dose of 10 μCi (diluted in PBS containing 0.1% BSA) through the tail vein.

Results are shown in Figure 23. Both the MuMc3 antibody (upper panel) and HuMc3 antibody (lower panel) concentrated at the tumor site, and persisted there throughout the period of the experiment. This confirms that the ability of HuMc3 to localize to the tumor site is comparable to that of the murine antibody from which it was derived, and that localization is independent of the method of labeling or the radioisotope used.

Claims

1. A recombinant Mc3 antibody which binds to BA46 antigen of the human milk fat globule (HMFG), said antibody comprising at least one modified variable region, said modified variable region selected from the group consisting of:

(i) a modified heavy chain variable region having an amino acid sequence substantially similar to that of murine Mc3 in Figure 12 in which at least one but fewer than about 30 of the amino acid residues of murine Mc3 have been substituted; and

(ii) a modified light chain variable region having an amino acid sequence substantially similar to that of murine Mc3 in Figure 13 in which at least one but fewer than about 30 of the amino acid residues of murine Mc3 have been substituted; and

(iii) a derivative of one of said modified variable regions in which one or more residues of the variable region that are not required for binding to the antigen have been deleted or in which one or more of the residues labelled (CDR) in Figure 12 or 13 have been modified without disrupting antigen binding.

2. A recombinant murine Mc3 antibody of claim 1, wherein at least one of said substituted amino acids is replaced with the corresponding amino acid from the appropriate human consensus sequence of Figure 12 or 13, for a heavy or light chain variable region, respectively.

3. A recombinant Mc3 antibody of claim 1 wherein said antibody comprises a heavy chain variable region and a light chain variable region.

4. A recombinant Mc3 antibody of claim 3 wherein both variable regions are modified variable regions, and wherein the antibody further comprises an antibody constant region or other effector agent.

5. A recombinant Mc3 antibody of claim 4 wherein the antibody comprises a constant region that is a human antibody constant region.

6. A recombinant Mc3 antibody of claim 1 wherein at least about five of the amino acid residues in one of said modified variable regions have been replaced with corresponding amino acids from the appropriate human consensus sequence of Figure 12 or 13, for a heavy or light chain variable region, respectively.

7. A recombinant Mc3 antibody of claim 1 comprising a modified heavy chain variable region in which at least about half of the residues listed as humanized or humanized (BR) in Figure 12 have been replaced with corresponding residues from the human consensus sequence of Figure 12.

8. A recombinant Mc3 antibody of claim 1 comprising a modified light chain variable region in which at least about half of the residues listed as humanized or humanized (BR) in Figure 13 have been replaced with corresponding residues from the human consensus sequence of Figure 13.

9. A recombinant Mc3 antibody of claim 5 comprising

a modified heavy chain variable region in which at least about 90% of the residues listed as humanized or humanized (BR) in Figure 12 have been replaced with corresponding residues from the human consensus sequence of Figure 12; and

a modified light chain variable region in which at least about 90% of the residues listed as humanized or humanized (BR) in Figure 13 have been replaced with corresponding residues from the human consensus sequence of Figure 13.

10. A recombinant Mc3 antibody of claim 9 in which all of the residues listed as humanized or humanized (BR) have been replaced with corresponding residues from the human consensus sequences of Figures 12 or 13, for the heavy and light chains respectively.

11. A pharmaceutical composition comprising a recombinant Mc3 antibody of claim 1 and a pharmaceutically acceptable carrier.

12. A nucleic acid sequence encoding a modified variable region of claim 1.

13. A nucleic acid sequence of claim 12 comprising the coding region of a modified variable region as shown in Figure 18 or 19.

14. An in vitro method of detecting the presence of an HMFG antigen or binding fragment thereof, comprising

obtaining a biological sample suspected of comprising the antigen or a fragment thereof;

adding a recombinant Mc3 antibody of claim 1 under conditions effective to form an antibody-antigen complex; and

detecting the presence of said antibody-antigen complex.

15. A method of diagnosing the presence of an HMFG antigen or binding fragment thereof in a subject, comprising

administering to the subject a recombinant Mc3 antibody of claim 1 under conditions effective to deliver it to an area of the subject's body suspected of containing an HMFG antigen or a binding fragment thereof to form an antibody-antigen complex; and

detecting the presence of said antibody-antigen complex.

16. A method of delivering an agent to a target site that contains an HMFG antigen comprising

binding said agent to a recombinant Mc3 antibody of claim 1 at a position other than the antigen binding site to create an agent-antibody complex; and

introducing the agent-antibody complex to the environment of said target site under conditions suitable for binding of an antibody to its cognate antigen.

17. A method of claim 16, wherein the target site is within the body of a human subject and introducing the agent-antibody complex comprises administering the complex to said subject.

18. A method of humanizing a non-human antibody comprising replacing one or more framework amino acid residues in a variable region of said antibody with corresponding framework amino acids from a human variable region wherein important non-human framework residues, as defined by the buried-residue-modification technique, are retained in their original form.

19. A method of humanizing a non-human antibody comprising replacing one or more framework amino acid residues in a variable region of said antibody with corresponding framework amino acids from a human variable region consensus sequence wherein important non-human framework residues, as defined by the buried-residue-modification technique, are retained in their original form.

20. A method of claim 19 wherein both the heavy and the light chain variable regions of said antibody are humanized.

FIGURE 1

Fab STRUCTURES FOR WHICH COORDINATES ARE IN THE PROTEIN DATA BANK

	ANTIBODY	RESOLUTION (A)	R-VALUE	PDB CODE
HUMAN:	NEWM	2.0	0.46	3FAB
	KOL	1.9	0.189	2FB4
MURINE:	McPC603	2.7	0.225	1MCP
	J539	1.95	0.194	2FBJ
	HyHEL-5	2.54	0.245	2HFL
	HyHEL-10	3.0	0.24	3HFM
	R19.9	2.8	0.30	1F19
	4-4-20	2.7	0.215	4FAB
	36-71	1.85	0.248	6FAB
	B13I2	2.8	0.197	1IGF
	D1.3	2.5	0.184	1FDL

FIGURE 2

V_L FRAMEWORK RESIDUES THAT CONTACT CDR RESIDUES IN Fabs OF KNOWN THREE-DIMENSIONAL STRUCTURE

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
1	GLU(2)	ASP(5)	ASP(10)	ASP(3)		ASP(8)	ASP(4)		ASP(11)		
2	ILE(11)	ILE(15)	ILE(17)	ILE(13)	ILE(5)	VAL(9)	ILE(20)	VAL(9)	ILE(10)	SER(3)	
3		VAL(3)	VAL(2)	VAL(3)	GLN(2)	VAL(2)	GLN(2)	LEU(6)		VAL(2)	
4	LEU(7)	MET(6)	LEU(6)	LEU(10)	MET(9)	MET(13)	MET(7)	MET(6)	MET(7)	LEU(4)	LEU(6)
5		THR(1)			THR(1)	THR(2)				THR(1)	
7								THR(4)			
22								SER(6)			
23	CYS(1)	CYS(1)	CYS(2)	CYS(2)	CYS(1)	CYS(1)	CYS(1)				CYS(1)
35	TRP(3)	TRP(2)	TRP(4)		TRP(2)		TRP(6)	TRP(4)	TRP(4)	TRP(1)	TRP(2)
36	TYR(12)	TYR(16)	TYR(8)	TYR(10)	TYR(22)	TYR(13)	TYR(15)	TYR(8)	TYR(14)	TYR(13)	TYR(11)
45					LYS(12)	LYS(5)					
46	PRO(3)	LEU(6)	LEU(4)	ARG(15)	LEU(5)	VAL(14)	LEU(5)	LEU(10)	LEU(6)	LEU(2)	LEU(6)
48	ILE(1)	ILE(1)	ILE(1)				ILE(3)	ILE(2)	VAL(1)		ILE(1)
49	TYR(28)	TYR(29)	LYS(13)	TYR(12)	TYR(40)	TYR(22)	TYR(22)	TYR(16)	TYR(25)		TYR(25)
58	VAL(3)	VAL(3)	ILE(1)	VAL(6)	VAL(6)	VAL(5)	VAL(4)	VAL(5)	VAL(1)		VAL(6)
60		ASP(1)				ASP(2)		ASP(4)			ASP(2)
62				PHE(1)		PHE(1)	PHE(1)				
66										LYS(2)	LYS(11)
67		SER(3)							SER(1)		
69		THR(3)	THR(3)			THR(5)	THR(1)	THR(4)	THR(1)	SER(1)	
70		ASP(2)			ASP(1)		ASP(6)			SER(2)	
71	TYR(14)	PHE(23)	PHE(17)	TYR(17)	TYR(24)	PHE(17)	TYR(17)	PHE(19)	TYR(16)	ALA(3)	ALA(4)
88	CYS(1)		CYS(2)		CYS(1)	CYS(1)	CYS(1)	CYS(1)	CYS(2)		CYS(1)
98	PHE(8)	PHE(8)	PHE(10)	PHE(5)	PHE(8)	PHE(4)	PHE(8)	PHE(14)	PHE(14)	PHE(3)	PHE(7)

FIGURE 3

V_H FRAMEWORK RESIDUES THAT CONTACT CDR RESIDUES IN Fabs OF KNOWN THREE-DIMENSIONAL STRUCTURE

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
1							GLU(3)				
2	VAL(11)	VAL(3)	VAL(8)		VAL(1)		VAL(7)	VAL(3)	VAL(12)		VAL(9)
4	LEU(2)	LEU(5)	LEU(5)		LEU(2)	LEU(1)	LEU(1)	LEU(1)	LEU(1)		LEU(1)
24		THR(2)	VAL(6)			ALA(1)					
27	PHE(3)	PHE(2)		TYR(14)	TYR(11)	PHE(26)	TYR(4)	PHE(4)	PHE(4)	THR(1)	PHE(3)
28	ASP(9)	THR(5)		THR(3)	THR(6)	THR(4)	THR(2)	THR(3)		SER(1)	ILE(2)
29	PHE(4)	PHE(4)		PHE(10)	PHE(7)	PHE(13)	PHE(6)	PHE(3)	LEU(1)		PHE(4)
30			THR(2)		THR(6)	SER(7)				ASP(6)	
36							TRP(2)				
37		VAL(1)			VAL(1)				VAL(1)	VAL(2)	VAL(1)
38	ARG(1)	ARG(2)	ARG(4)	LYS(2)	LYS(1)	ARG(4)	LYS(2)	ARG(1)			ARG(3)
40				ARG(1)							
46	GLU(3)	GLU(4)	GLU(1)	GLU(27)	GLU(3)	GLU(4)	GLU(9)		GLU(1)		GLU(1)
47	TRP(21)	TRP(29)	TYR(20)	TRP(21)	TRP(13)	TRP(18)	TRP(21)	TRP(23)	TRP(19)	TRP(22)	TRP(15)
48	ILE(1)	ILE(1)	MET(6)	ILE(12)	ILE(13)	VAL(1)	ILE(9)	VAL(3)	LEU(1)	ILE(2)	VAL(1)
49		ALA(2)				ALA(2)		ALA(2)			ALA(2)
66			ARG(11)			ARG(3)		ARG(2)		ARG(2)	ARG(1)
67	PHE(4)	PHE(10)	ILE(9)	ALA(1)		PHE(11)	THR(5)	PHE(12)	LEU(6)	VAL(2)	PHE(10)
68		ILE(1)			THR(1)	THR(11)					THR(2)
69	ILE(8)	VAL(6)	ILE(8)	PHE(12)	LEU(5)	ILE(20)	LEU(6)	ILE(11)	ILE(8)	MET(4)	ILE(9)
71	ARG(7)	ARG(16)	ARG(2)	ALA(1)	VAL(4)	ARG(6)	VAL(6)	ARG(3)	LYS(4)		ARG(9)
73	ASN(1)	THR(3)				ASP(3)					
78	LEU(4)	LEU(7)	TYR(9)	ALA(1)	ALA(1)	VAL(2)	ALA(1)	LEU(6)	VAL(4)	PHE(5)	LEU(5)
80						LEU(1)					
82			LEU(2)						MET(1)	LEU(1)	
86						ASP(2)					
92				CYS(1)			CYS(1)		CYS(1)		
93	ALA(4)	ALA(5)		LEU(2)		THR(3)	ALA(1)	THR(5)	ALA(4)	ALA(1)	ALA(3)
94	ARG(38)	ARG(24)	ASN(11)	HIS(2)	ARG(30)		ARG(23)	ARG(14)	ARG(30)	ARG(22)	ARG(27)
103	TRP(5)	TRP(9)			TRP(2)	TRP(2)	TRP(5)		TRP(2)	TRP(4)	TRP(4)

FIGURE 4

FRAMEWORK RESIDUES THAT CONTACT FRAMEWORK RESIDUES IN THE OPPOSITE DOMAIN IN Fabs OF KNOWN THREE-DIMENSIONAL STRUCTURE

IN V_L:

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
36	TYR(3)	TYR(4)	TYR(3)	TYR(5)		TYR(11)	TYR(7)	TYR(1)	TYR(7)		TYR(5)
38	GLN(10)	GLN(4)	GLN(9)	GLN(5)	GLN(5)	GLN(3)	GLN(6)	GLN(12)	GLN(6)	GLN(7)	GLN(8)
43	SER(7)	PRO(1)	SER(8)	SER(5)	THR(3)			SER(3)	SER(2)	ALA(5)	ALA(1)
44	PRO(10)	PRO(14)	PRO(8)	PRO(11),		PRO(7)	ILE(20)	PRO(16)	PRO(16)	PRO(7)	PRO(13)
46	PRO(3)										
85			MET(2)		THR(5)			VAL (1)		ASP(12)	
87	TYR(6)	TYR(4)	PHE(6)	TYR(2)			PHE(5)	TYR(10)	TYR(8)	TYR(6)	TYR(6)
98	PHE(11)	PHE(8)	PHE(7)	PHE(12)	PHE(12)	PHE(12)	PHE(8)	PHE(13)	PHE(12)	PHE(10)	PHE(15)
100		ALA(2)									

IN V_H:

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
37	VAL(4)		ILE(2)	VAL(1)	VAL(4)	VAL(2)	VAL(1)	VAL(2)	VAL(4)	VAL(1)	VAL(4)
39	GLN(10)	GLN(4)	LYS(8)	GLN(5)	GLN(5)	GLN(3)	GLN(6)	GLN(10)	GLN(6)	GLN(4)	GLN(7)
43			ASN(4)		GLN(7)			LYS(6)		ARG(19)	
44		ARG(2)									
45	LEU(13)	LEU(12)	LEU(8)	LEU(14)		LEU(8)	LEU(11)	LEU(13)	LEU(14)	LEU(11)	LEU(16)
47	TRP(1)		TYR(2)		TRP(2)				TRP(3)	TRP(2)	
91	TYR(6)	TYR(4)	TYR(3)	TYR(8)	PHE(3)	TYR(2)	PHE(4)	TYR(3)	TYR(5)	TYR(3)	
103	TRP(11)	TRP(15)	TRP(16)	TRP(11)	TRP(4)	TRP(18)	TRP(24)	TRP(22)	TRP(19)	TRP(8)	TRP(19)
105	GLN(5)										

FIGURE 5

INWARD-POINTING, BURIED FRAMEWORK RESIDUES IN THE V_L OF Fabs OF KNOWN THREE-DIMENSIONAL STRUCTURE

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
2	ILE	ILE	ILE	ILE	ILE	VAL	ILE	VAL	ILE		
4	LEU	MET	LEU	LEU	MET	MET	MET	MET	MET	LEU	LEU
6	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN
11	THR	LEU	LEU	MET	LEU	LEU	LEU	LEU	LEU	VAL	ALA
13	ALA	VAL	VAL	ALA	ALA	VAL	ALA	VAL	ALA		
19	VAL	VAL	VAL	VAL	VAL	ALA	VAL	ALA	VAL	VAL	VAL
21	ILE	MET	LEU	MET	ILE	ILE	ILE	ILE	ILE	ILE	ILE
23	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
35	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
37	GLN	GLN	GLN	GLN	GLN	LEU	GLN	LEU	GLN	GLN	GLN
47	TRP	LEU	LEU	TRP	LEU	LEU	LEU	LEU	LEU	LEU	LEU
48	ILE	ILE	ILE	ILE	VAL	ILE	ILE	ILE	VAL		ILE
49										PHE	
58	VAL	VAL	ILE	VAL	VAL	VAL	VAL	VAL	VAL		VAL
61	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG		ARG
62	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE	PHE
71	TYR	PHE	PHE	TYR	TYR	PHE	TYR	PHE	TYR	ALA	ALA
73	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
75	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
78	MET	VAL	VAL	MET	LEU	VAL	LEU	VAL	LEU	LEU	LEU
82	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
83									PHE		
84	ALA	ALA		ALA	ALA		ALA			ALA	THR
86	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
88	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
102	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
104	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	VAL
106	LEU	ILE	ILE	ILE			ILE	ILE		VAL	VAL

FIGURE 6

INWARD-POINTING, BURIED FRAMEWORK RESIDUES IN THE V_K OF Fabs OF KNOWN THREE-DIMENSIONAL STRUCTURE

POSITION	ANTIBODY										
	J539	McPC603	HyHEL-10	HyHEL-5	R19.9	4-4-20	36-71	B13I2	D1.3	NEWM	KOL
2	VAL	VAL	VAL				VAL	VAL	VAL		VAL
4	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
6	GLU	GLU	GLU	GLN	GLU	GLU	GLN	GLU	GLU	GLN	GLN
9			PRO								
12	VAL	VAL	VAL	MET	VAL	VAL	VAL	VAL	VAL	VAL	VAL
18	LEU	LEU	LEU	VAL	VAL	MET	VAL	LEU	LEU	LEU	LEU
20	LEU	LEU	LEU	ILE	MET	LEU	MET	LEU	ILE	LEU	LEU
22	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
24	ALA	THR	VAL	ALA	ALA	ALA	ALA	ALA	VAL	VAL	SER
27	PHE	PHE	ASP	TYR	TYR	PHE	TYR	PHE	PHE	THR	PHE
29	PHE	PHE	ILE	PHE	PHE	PHE	PHE	PHE	LEU	PHE	PHE
36	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP	TRP
38	ARG	ARG	ARG	LYS	LYS	ARG	LYS	ARG	ARG	ARG	ARG
40						SER					
46		GLU	GLU	GLU							
48	ILE	ILE	MET	ILE	ILE	VAL	ILE	VAL	LEU	ILE	VAL
49		ALA				ALA		ALA			ALA
66	LYS	ARG	ARG	LYS				ARG	ARG	ARG	ARG
67	PHE	PHE	ILE	ALA	THR	PHE	THR	PHE	LEU	VAL	PHE
69	ILE	VAL	ILE	PHE	LEU	ILE	LEU	ILE	ILE	MET	ILE
71	ARG	ARG	ARG	ALA	VAL	ARG	VAL	ARG	LYS	VAL	ARG
76						SER					
78	LEU	LEU	TYR	ALA	ALA	VAL	ALA	LEU	VAL	PHE	LEU
80	LEU	LEU	LEU	MET	MET	LEU	MET	LEU	LEU	LEU	LEU
82	MET	MET	LEU	LEU	LEU	MET	LEU	MET	MET	LEU	MET
82C	VAL	LEU	VAL	LEU	LEU	LEU	LEU	LEU	LEU	VAL	LEU
86	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
88	ALA	ALA	ALA		ALA		ALA	ALA	ALA	ALA	
90	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR	TYR
92	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS	CYS
94	ARG	ARG	ASN	HIS	ARG		ARG	ARG	ARG	ARG	ARG
107	THR	THR		THR	THR	THR	THR	THR	THR	SER	THR
109	VAL	VAL	VAL	LEU	LEU	VAL	LEU	LEU	LEU	VAL	VAL
111	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL

FIGURE 7

HUMAN ANTIBODIES THAT ARE MOST SIMILAR IN SEQUENCE TO MURINE ANTIBODIES OF KNOWN THREE-DIMENSIONAL STRUCTURE

ANTIBODY	DOMAIN	MOST SIMILAR HUMAN SEQUENCE
HyHEL-10	VH	58P2'CL (77/112)
	VH FRAMEWORK	15P1'CL, ML1'CL (62/87)
	VH IMPT	58P2'CL, Ab26'CL, C6B2'CL (28/38)
	VL	IARC/BL41'CL (73/107)
	VL FRAMEWORK	IARC/BL41'CL (59/80)
	VL IMPT	IARC/BL41'CL (30/37)
HyHEL-5	VH	ND'CL (74/116)
	VH FRAMEWORK	783c'CL, X17115'CL (63/87)
	VH IMPT	21/28'CL, 51P1'CL, 783c'CL, 8E10'CL, AND, KAS, NEI'CL, X17115'CL (25/37)
	VL	HF2-1/17'CL, KAS (65/105)
	VL FRAMEWORK	HF2-1/17'CL (57/80)
	VL IMPT	BI, DEN, HF2-1/17'CL, KUE, REI, WALKER'CL, WIL(-) (27/36)
R19.9	VH	21/28'CL (73/119)
	VH FRAMEWORK	21/28'CL, 51P1'CL, AND, LS2'CL, NEI'CL (60/87)
	VH IMPT	21/28'CL, 8E10'CL, LS2'CL (28/38)
	VL	WALKER'CL (78/107)
	VL FRAMEWORK	RZ (62/80)
	VL IMPT	REI, WALKER'CL (33/36)

FIGURE 7A

4-4-20	VH	30P1'CL (77/116)
	VH FRAMEWORK	2P1'CL, 3D6'CL (65/87)
	VH IMPT	4B4'CL, M26'CL (36/41)
	VL	RPMI-6410'CL (91/112)
	VL FRAMEWORK	GM-607-'CL (68/80)
	VL IMPT	CUM, FR, NIM (33/36)
J539	VH	30P1'CL, Vh38C1.10'CL (81/118)
	VH FRAMEWORK	18/2'CL, 30P1'CL, M43 (71/87)
	VH IMPT	30P1'CL, 56P1'CL, M72, M74 (36/40)
	VL	PA (62/105)
	VL FRAMEWORK	LEN, WEA (53/80)
	VL IMPT	BI, DEN, KUE, REI, WALKER'CL, WIL(-) (26/35)
McPC603	VH	M72 (81/120)
	VH FRAMEWORK	4G12'CL, Ab18'CL, M72 (70/87)
	VH IMPT	56P1'CL, M72, M74, RF-SJ2'CL (36/42)
	VL	FK-001'CL, LEN (91/113)
	VL FRAMEWORK	LEN (70/80)
	VL IMPT	LEN (38/42)
36-71	VH	21/28'CL (74/119)
	VH FRAMEWORK	21/28'CL, 51P1'CL, 703c'CL, AND'CL, NEI'CL, X17115'CL, (61/87)
	VH IMPT	21/28'CL, 8E10'CL (28/38)
	VL	AG (76/105)
	VL FRAMEWORK	RZ (63/80)
	VL IMPT	REI, RZ, WALKER'CL (34/37)

FIGURE 7B

B1312	VH	
	VH FRAMEWORK	56P1'CL (83/119)
	VH IMPT	4B4'CL, 4G12'CL, M26'CL, M72, RF-SJ2'CL, Vh38C1.10'CL (68/87)
		56P1'CL, M72, M74, RF-SJ2'CL (37/39)
	VL	
	VL FRAMEWORK	RPM1-6410'CL (86/112)
	VL IMPT	GM-607-'CL (69/80)
		CUM, NIM (36/39)
D1.3	VH	
	VH FRAMEWORK	C6B2'CL (72/116)
	VH IMPT	C6B2'CL (62/87)
		M60'CL (32/37)
	VL	
	VL FRAMEWORK	BR (75/107)
	VL IMPT	HF2-1/17'CL (64/80)
		3D6'CL, BI, DEN, EU, KUE, PA, REI, WALKER'CL, WIL(-) (32/36)

FIGURE 8

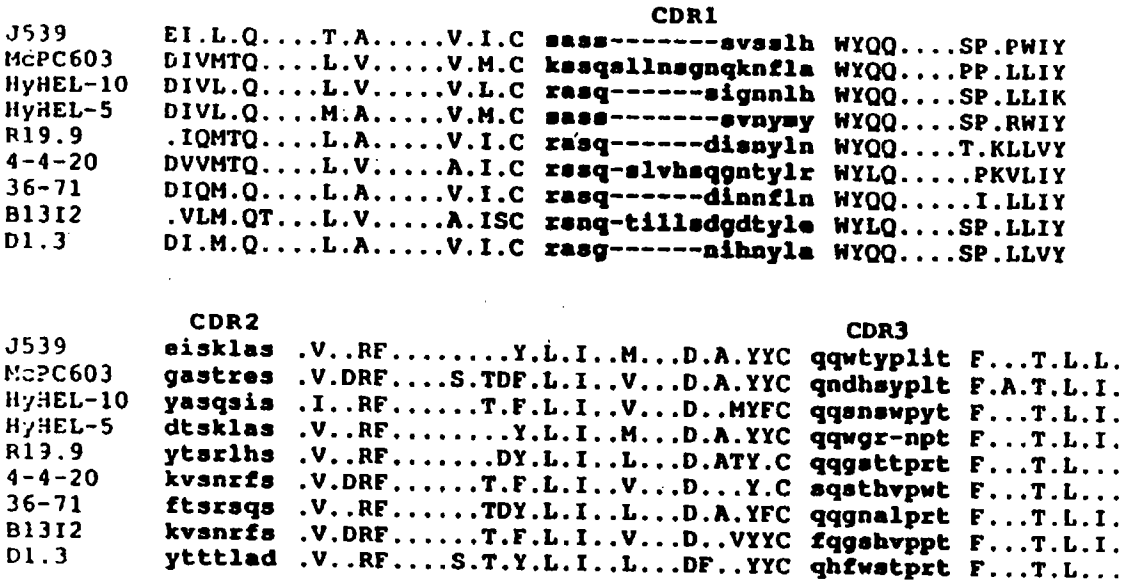

CDR1
J539 EI.L.Q....T.A.....V.I.C sass-------svsslh WYQQ....SP.PWIY
McPC603 DIVMTQ....L.V.....V.M.C kssqsllnsgnqknfla WYQQ....PP.LLIY
HyHEL-10 DIVL.Q....L.V.....V.L.C rasq------signnlh WYQQ....SP.LLIK
HyHEL-5 DIVL.Q....M.A.....V.M.C sass-------svnymy WYQQ....SP.RWIY
R19.9 .IQMTQ....L.A.....V.I.C ra'sq------disnyln WYQQ....T.KLLVY
4-4-20 DVVMTQ....L.V.....A.I.C rssq-slvhsqgntylr WYLQ.....PKVLIY
36-71 DIQM.Q....L.A.....V.I.C rasq------dinnfln WYQQ.....I.LLIY
B13I2 .VLM.QT...L.V.....A.ISC rsnq-tillsdgdtyle WYLQ....SP.LLIY
D1.3 DI.M.Q....L.A.....V.I.C rasg------nihnyla WYQQ....SP.LLVY
CDR2
CDR3
J539 eisklas .V..RF.....Y.L.I..M...D.A.YYC qqwtyplit F...T.L.L.
McPC603 gastres .V.DRF....S.TDF.L.I..V...D.A.YYC qndhsyplt F.A.T.L.I.
HyHEL-10 yasqsis .I..RF.....T.F.L.I..V...D..MYFC qqsnswpyt F...T.L.I.
HyHEL-5 dtsklas .V..RF.....Y.L.I..M...D.A.YYC qqwgr-npt F...T.L.I.
R19.9 ytsrlhs .V..RF.....DY.L.I..L...D.ATY.C qqgsttprt F...T.L...
4-4-20 kvsnrfs .V.DRF.....T.F.L.I..V...D...Y.C sqsthvpwt F...T.L...
36-71 ftsrsqs .V..RF.....TDY.L.I..L...D.A.YFC qqgnalprt F...T.L.I.
B13I2 kvsnrfs .V.DRF.....T.F.L.I..V...D..VYYC fqgshvppt F...T.L.I.
D1.3 ytttlad .V..RF....S.T.Y.L.I..L...DF..YYC qhfwstprt F...T.L...

FIGURE 9

Framework Residues In V_H That Probably Need To Be Preserved In Order To Reproduce The Ligand Binding Properties Of The Original Antibody

		CDR1	
J539	.V.L.E.....V.....L.L.C.A..FDF.	kywms	WVRQ.....LEWI.
McPC603	.V.L.E.....V.....L.L.C.T..FTF.	dfyme	WVRQ....RLEWIA
HyHEL-10	.V.L.E..P..V.....L.L.C.V..D.IT	sdyws	WIRK...N.LEYM.
HyHEL-5	...L.Q.....M.....V.I.C.A..YTF.	dywie	WVKQR....LEWI.
R19.9	.V.L.E.....V.....V.M.C.A..YTFT	sygvn	WVKQ...Q..EWI.
4-4-20	...L.E.....V.....M.L.C.A..FTFS	dywmn	WVRQS....LEWVA
36-71	EV.L.Q.....V.....V.M.C.A..YTF.	sngin	WVKQ.....LEWI.
B13I2	.V.L.E.....V.....L.L.C.A..FTF.	rcams	WVRQ...K.L.WVA
D1.3	.V.L.E.....V.....L.I.C.V..F.L.	gygvn	WVRQ.....LEWL.

	CDR2	
J539	eihp--dsgtinytpslkd	KF.I.R.N....L.L.M..V...D.A.YYCAR
McPC603	asrnkgnkytteysasvkg	RFIV.R.T....L.L.M..L...D.A.YYCAR
HyHEL-10	yvs---ysgstyynpslks	RI.I.R......Y.L.L..V...D.A.YYC.N
HyHEL-5	eilp--gsgstnyherfkg	KA.F.A......A.M.L..L...D...YYCLH
R19.9	yinp--gkgylsynekfkg	.TTL.V......A.M.L..L...D.A.YFC.R
4-4-20	qirnkpynyetyysdsvkg	RFTI.R.D..S.V.L.M..L...D...YYCT.
36-71	ynnp--gngyiaynekfkg	.T.L.V......A.M.L..L...D.A.YFCAR
B13I2	giss--ggsytfypdtvkg	RF.I.R......L.L.M..L...D.A.YYCTR
D1.3	miw---gdgntdynsalks	RL.I.K......V.L.M..L...D.A.YYCAR

	CDR3	
J539	lhyygyn------ay	W.Q.T.V.V..
McPC603	nyygstwyf----dv	W...T.V.V..
HyHEL-10	wdg----------dy	W.....V.V..
HyHEL-5	gnydf--------dg	W...T.L.V..
R19.9	sfyggsdlavyyfds	W...T.L.V..
4-4-20	syygm--------dy	W...T.V.V..
36-71	seyyggsykf---dy	W...T.L.V..
B13I2	yssdpfyf-----dy	W...T.L.V..
D1.3	erdyrl-------dy	W...T.L.V..

Figure 10: MuMc3 V_H

```
atg aaa tgc agc tgg gtc att ctc ttC CTC CTG TCA GGA ACT GCA GGT GTC CAC
m   k   c   s   w   v   i   l   f   l   l   s   g   t   a   g   v   h

TCT GAG GTC CAG CTG CAA CAG TCT GGA CCT GAG CTG GTG AAG CCT GGA GCT TCA
s   E   V   Q   L   Q   Q   S   G   P   E   L   V   K   P   G   A   S

ATG AAG ATA TCC TGC GAG GCT TCT GGT TAC TCA TTC ACT GGC TAT ACC ATG CAC
M   K   I   S   C   E   A   S   G   Y   S   F   T   G   Y   T   M   H

TGG GTG AAG CAG AGC CAT GGA ATG AAC CTT GAG TGG ATT GGA CTT ATT AAT CCT
W   V   K   Q   S   H   G   M   N   L   E   W   I   G   L   I   N   P

TAC AAT GGT GGT ACT GTC TAC AAC CAG AAG TTC CAG GAC AAG GCC ACA TTA ACT
Y   N   G   G   T   V   Y   N   Q   K   F   Q   D   K   A   T   L   T

GTA GAC AAG TCA TCC GGC ACA GCC TAC ATG GAG CTC CTC AGT CTG ACA TCT GAG
V   D   K   S   S   G   T   A   Y   M   E   L   L   S   L   T   S   E

GAC TCT GCA GTC TAT TTC TGT GCA AGA CGT TGG AGA TAT ACT ATG GAC TAT TGG
D   S   A   V   Y   F   C   A   R   R   W   R   Y   T   M   D   Y   W

GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA G
G   Q   G   T   S   V   T   V   S   S
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Figure 11: MuMc3 V_K

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atg gag ttc cag acc cag gtC TTT GTA TTC GTG TTT CTC TGG TTG TCT GGT GTT
m   e   f   q   t   q   v   f   v   f   v   f   l   w   l   s   g   v

GAC GGA GAC ATT GTG ATG ACC CAG TCT CAC AAA TTC ATG TCC ACA TCA GAG GGA
d   g   D   I   V   M   T   Q   S   H   K   F   M   S   T   S   E   G

GAC TGG GTC AGC ATC ACC TGC AAG GCC AGT CAG GAT GTG AGT ATT GGT GTA GCC
D   W   V   S   I   T   C   K   A   S   Q   D   V   S   I   G   V   A

TGG TAT CAA CAG AAA CCA GGA CAA TCT CCT AAA CTG CTG ATT TAC TCG GCA TCC
W   Y   Q   Q   K   P   G   Q   S   P   K   L   L   I   Y   S   A   S

TCC CGG TAC ACT GGA GTC CCT GAT CGC TTC AGT GGC AGT GGA TCT GGG ACG GAT
S   R   Y   T   G   V   P   D   R   F   S   G   S   G   S   G   T   D

TTC ACT TTC ACC ATC AGC AGT GTG CAG GCT GAA GAC CTG GCA GTT TAT TAC TGT
F   T   F   T   I   S   S   V   Q   A   E   D   L   A   V   Y   Y   C

CAG CAA CAT TAT ACT TCT CCA TTC ACG TTC GGC TCG GGG ACA AAC TTG GAA ATA
Q   Q   H   Y   T   S   P   F   T   F   G   S   G   T   N   L   E   I

AAA C
K
```

V_H	Murine MC3	Human Consensus (V_HI)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
1	E	Q	Yes (contact CDR)	Not humanized	E
2	V	V	Yes (same as human)	n/a	V
3	Q	Q	Yes (same as human)	n/a	Q
4	L	L	Yes (same as human)	n/a	L
5	Q	V	No	Humanized	V
6	Q	Q	Yes (same as human)	n/a	Q
7	S	S	Yes (same as human)	n/a	S
8	G	G	Yes (same as human)	n/a	G
9	P	A	No	Humanized (BR)	A
10	E	E	Yes (same as human)	n/a	E
11	L	V	No	Humanized	V
12	V	K	No	Humanized (BR)	K
13	K	K	Yes (same as human)	n/a	K
14	P	P	Yes (same as human)	n/a	P
15	G	G	Yes (same as human)	n/a	G
16	A	A	Yes (same as human)	n/a	A
17	S	S	Yes (same as human)	n/a	S
18	M	V	No	Humanized (BR)	V
19	K	K	Yes (same as human)	n/a	K
20	I	V	No	Humanized (BR)	V
21	S	S	Yes (same as human)	n/a	S
22	C	C	Yes (same as human)	n/a	C
23	E	K	No	Humanized	K
24	A	A	Yes (same as human)	n/a	A
25	S	S	Yes (same as human)	n/a	S
26	G	G	Yes (same as human)	n/a	G
27	Y	Y	Yes (same as human)	n/a	Y
28	S	T	Yes (contact CDR)	Not humanized	S
29	F	F	Yes (same as human)	n/a	F
30	T	T	Yes (same as human)	n/a	T
31	G	S	Yes (CDR)	Not humanized	G
32	Y	Y	Yes (CDR)	n/a	Y

Figure 12 - 1

V_H	Murine MC3	Human Consensus (V_HI)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
33	T	A	Yes (CDR)	Not humanized	T
34	M	I	Yes (CDR)	Not humanized	M
35	H	S	Yes (CDR)	Not humanized	H
36	W	W	Yes (same as human)	n/a	W
37	V	V	Yes (same as human)	n/a	V
38	K	R	Yes (contact CDR)	Not humanized	K
39	Q	Q	Yes (same as human)	n/a	Q
40	S	A	Yes (contact CDR)	Not humanized	S
41	H	P	No	Humanized	P
42	G	G	Yes (same as human)	n/a	G
43	M	Q	Yes (interchain cont.)	Not humanized	M
44	N	G	Yes (interchain cont.)	Not humanized	N
45	L	L	Yes (same as human)	n/a	L
46	E	E	Yes (same as human)	n/a	E
47	W	W	Yes (same as human)	n/a	W
48	I	M	Yes (contact CDR)	Not humanized	I
49	G	G	Yes (same as human)	n/a	G
50	L	W	Yes (CDR)	Not humanized	L
51	I	I	Yes (CDR)	n/a	I
52	N	N	Yes (CDR)	n/a	N
52a	P	P	Yes (CDR)	n/a	P
52b	Y	Y	Yes (CDR)	n/a	Y
53	N	G	Yes (CDR)	Not humanized	N
54	G	N	Yes (CDR)	Not humanized	G
55	G	G	Yes (CDR)	n/a	G
56	-	D	Yes (CDR)	Not humanized	-
57	T	T	Yes (CDR)	n/a	T
58	V	N	Yes (CDR)	Not humanized	V
59	Y	Y	Yes (CDR)	n/a	Y
60	N	A	Yes (CDR)	Not humanized	N
61	Q	Q	Yes (CDR)	n/a	Q
62	K	K	Yes (CDR)	n/a	K

Figure 12 - 2

V_H	Murine MC3	Human Consensus (V_HI)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
63	F	F	Yes (CDR)	n/a	F
64	Q	Q	Yes (CDR)	n/a	Q
65	D	G	Yes (CDR)	Not humanized	D
66	K	R	Yes (contact CDR)	Not humanized	K
67	A	V	Yes (contact CDR)	Not humanized	A
68	T	T	Yes (same as human)	n/a	T
69	L	I	Yes (contact CDR)	Not humanized	L
70	T	T	Yes (same as human)	n/a	T
71	V	A	Yes (contact CDR)	Not humanized	V
72	D	D	Yes (same as human)	n/a	D
73	K	T	Yes (contact CDR)	Not humanized	K
74	S	S	Yes (same as human)	n/a	S
75	S	T	No	Humanized	T
76	G	S	No	Humanized (BR)	S
77	T	T	Yes (same as human)	n/a	T
78	A	A	Yes (same as human)	n/a	A
79	Y	Y	Yes (same as human)	n/a	Y
80	M	M	Yes (same as human)	n/a	M
81	E	E	Yes (same as human)	n/a	E
82	L	L	Yes (same as human)	n/a	L
82a	L	S	No	Humanized	S
82b	S	S	Yes (same as human)	n/a	S
82c	L	L	Yes (same as human)	n/a	L
83	T	R	No	Humanized	R
84	S	S	Yes (same as human)	n/a	S
85	E	E	Yes (same as human)	n/a	E
86	D	D	Yes (same as human)	n/a	D
87	S	T	No	Humanized	T
88	A	A	Yes (same as human)	n/a	A
89	V	V	Yes (same as human)	n/a	V
90	Y	Y	Yes (same as human)	n/a	Y
91	F	Y	Yes (interchain cont.)	Not humanized	F

Figure 12 - 3

V_H	Murine MC3	Human Consensus (V_HI)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
92	C	C	Yes (same as human)	n/a	C
93	A	A	Yes (same as human)	n/a	A
94	R	R	Yes (same as human)	n/a	R
95	R	A	Yes (CDR)	Not humanized	R
96	-	P	Yes (CDR)	Not humanized	-
97	-	G	Yes (CDR)	Not humanized	-
98	-	Y	Yes (CDR)	Not humanized	-
99	-	G	Yes (CDR)	Not humanized	-
100	-	S	Yes (CDR)	Not humanized	-
100a	-	G	Yes (CDR)	Not humanized	-
100b	-	G	Yes (CDR)	Not humanized	-
100c	-	G	Yes (CDR)	Not humanized	-
100d	-	C	Yes (CDR)	Not humanized	-
100e	W	Y	Yes (CDR)	Not humanized	W
100f	R	R	Yes (CDR)	n/a	R
100g	-	G	Yes (CDR)	Not humanized	-
100h	-	D	Yes (CDR)	Not humanized	-
100i	Y	Y	Yes (CDR)	n/a	Y
100j	T	X	Yes (CDR)	Not humanized	T
100k	M	F	Yes (CDR)	Not humanized	M
101	D	D	Yes (CDR)	n/a	D
102	Y	Y	Yes (CDR)	n/a	Y
103	W	W	Yes (same as human)	n/a	W
104	G	G	Yes (same as human)	n/a	G
105	Q	Q	Yes (same as human)	n/a	Q
106	G	G	Yes (same as human)	n/a	G
107	T	T	Yes (same as human)	n/a	T
108	S	L	No	Humanized	L
109	V	V	Yes (same as human)	n/a	V
110	T	T	Yes (same as human)	n/a	T
111	V	V	Yes (same as human)	n/a	V
112	S	S	Yes (same as human)	n/a	S

Figure 12 - 4

V_H	Murine MC3	Human Consensus (V_HI)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
113	S	S	Yes (same as human)	n/a	S

Figure 12 - 5

V_K	Murine MC3	Human Consensus (V_KIV)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
1	D	D	Yes (same as human)	n/a	D
2	I	I	Yes (same as human)	n/a	I
3	V	V	Yes (same as human)	n/a	V
4	M	M	Yes (same as human)	n/a	M
5	T	T	Yes (same as human)	n/a	T
6	Q	Q	Yes (same as human)	n/a	Q
7	S	S	Yes (same as human)	n/a	S
8	H	P	No	Humanized	P
9	K	D	No	Humanized	D
10	F	S	No	Humanized	S
11	M	L	No	Humanized (BR)	L
12	S	A	No	Humanized	A
13	T	V	No	Humanized (BR)	V
14	S	S	Yes (same as human)	n/a	S
15	E	L	No	Humanized	L
16	G	G	Yes (same as human)	n/a	G
17	D	E	No	Humanized	E
18	W	R	No	Humanized	R
19	V	A	No	Humanized (BR)	A
20	S	T	No	Humanized	T
21	I	I	Yes (same as human)	n/a	I
22	T	N	Yes (contact CDR)	Not humanized	T
23	C	C	Yes (same as human)	n/a	C
24	K	K	Yes (CDR)	n/a	K
25	A	S	Yes (CDR)	Not humanized	A
26	S	S	Yes (CDR)	n/a	S
27	Q	Q	Yes (CDR)	n/a	Q
27a	D	S	Yes (CDR)	Not humanized	D
27b	V	V	Yes (CDR)	n/a	V
27c	S	L	Yes (CDR)	Not humanized	S
27d	I	Y	Yes (CDR)	Not humanized	I
27e	G	S	Yes (CDR)	Not humanized	G

Figure 13 - 1

V_K	Murine MC3	Human Consensus (V_KIV)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
27f	-	S	Yes (CDR)	Not humanized	-
28	-	N	Yes (CDR)	Not humanized	-
29	-	N	Yes (CDR)	Not humanized	-
30	-	K	Yes (CDR)	Not humanized	-
31	-	N	Yes (CDR)	Not humanized	-
32	-	Y	Yes (CDR)	Not humanized	-
33	V	L	Yes (CDR)	Not humanized	V
34	A	A	Yes (CDR)	n/a	A
35	W	W	Yes (same as human)	n/a	W
36	Y	Y	Yes (same as human)	n/a	Y
37	Q	Q	Yes (same as human)	n/a	Q
38	Q	Q	Yes (same as human)	n/a	Q
39	K	K	Yes (same as human)	n/a	K
40	P	P	Yes (same as human)	n/a	P
41	G	G	Yes (same as human)	n/a	G
42	Q	Q	Yes (same as human)	n/a	Q
43	S	P	Yes (interchain cont.)	Not humanized	S
44	P	P	Yes (same as human)	n/a	P
45	K	K	Yes (same as human)	n/a	K
46	L	L	Yes (same as human)	n/a	L
47	L	L	Yes (same as human)	n/a	L
48	I	I	Yes (same as human)	n/a	I
49	Y	Y	Yes (same as human)	n/a	Y
50	S	W	Yes (CDR)	Not humanized	S
51	A	A	Yes (CDR)	n/a	A
52	S	S	Yes (CDR)	n/a	S
53	S	T	Yes (CDR)	Not humanized	S
54	R	R	Yes (CDR)	n/a	R
55	Y	E	Yes (CDR)	Not humanized	Y
56	T	S	Yes (CDR)	Not humanized	T
57	G	G	Yes (same as human)	n/a	G
58	V	V	Yes (same as human)	n/a	V

Figure 13 - 2

V_K	Murine MC3	Human Consensus (V_KIV)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
59	P	P	Yes (same as human)	n/a	P
60	D	D	Yes (same as human)	n/a	D
61	R	R	Yes (same as human)	n/a	R
62	F	F	Yes (same as human)	n/a	F
63	S	S	Yes (same as human)	n/a	S
64	G	G	Yes (same as human)	n/a	G
65	S	S	Yes (same as human)	n/a	S
66	G	G	Yes (same as human)	n/a	G
67	S	S	Yes (same as human)	n/a	S
68	G	G	Yes (same as human)	n/a	G
69	T	T	Yes (same as human)	n/a	T
70	D	D	Yes (same as human)	n/a	D
71	F	F	Yes (same as human)	n/a	F
72	T	T	Yes (same as human)	n/a	T
73	F	L	No	Humanized (BR)	L
74	T	T	Yes (same as human)	n/a	T
75	I	I	Yes (same as human)	n/a	I
76	S	S	Yes (same as human)	n/a	S
77	S	S	Yes (same as human)	n/a	S
78	V	L	No	Humanized (BR)	L
79	Q	Q	Yes (same as human)	n/a	Q
80	A	A	Yes (same as human)	n/a	A
81	E	E	Yes (same as human)	n/a	E
82	D	D	Yes (same as human)	n/a	D
83	L	V	No	Humanized (BR)	V
84	A	A	Yes (same as human)	n/a	A
85	V	V	Yes (same as human)	n/a	V
86	Y	Y	Yes (same as human)	n/a	Y
87	Y	Y	Yes (same as human)	n/a	Y
88	C	C	Yes (same as human)	n/a	C
89	Q	Q	Yes (CDR)	n/a	Q
90	Q	Q	Yes (CDR)	n/a	Q

Figure 13 - 3

V_K	Murine MC3	Human Consensus (V_KIV)	Humanization Protocol		Humanized MC3
			Murine Retained	Humanized	
91	H	Y	Yes (CDR)	Not humanized	H
92	Y	Y	Yes (CDR)	n/a	Y
93	T	S	Yes (CDR)	Not humanized	T
94	S	T	Yes (CDR)	Not humanized	S
95	P	P	Yes (CDR)	n/a	P
96	F	X	Yes (CDR)	Not humanized	F
97	T	T	Yes (CDR)	n/a	T
98	P	P	Yes (same as human)	n/a	P
99	G	G	Yes (same as human)	n/a	G
100	S	Q	Yes (interchain cont.)	Not humanized	S
101	G	G	Yes (same as human)	n/a	G
102	T	T	Yes (same as human)	n/a	T
103	N	K	No	Humanized	K
104	L	V	No	Humanized (BR)	V
105	E	E	Yes (same as human)	n/a	E
106	I	I	Yes (same as human)	n/a	I
107	K	K	Yes (same as human)	n/a	K

Figure 13 - 4

Figure 14: HuMc3 V_H (BR-R version)

```
mkcsw vilfl lsgta gvhsE VQLVQ SGPEV VKPGA SMKIS CKASG YSFTG   50

YTMH WVKQSP GMNLE WIGLI NPYNG GTVYN QKFQD KATLT VDKST GTAYM  100

ELSSL RSEDT AVYFC ARRWR YTMDY WGQGT LVTVS S                  136
```

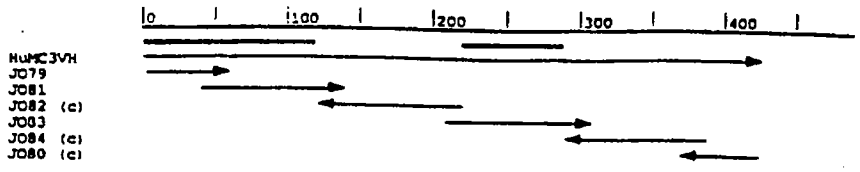
Figure 15: HuMc3 V_κ (BR-R version)

```
mefqt qvfvf vflwl sgvdg DIVMT QSPDS MATSL GERVT ITCKA SQDVS   50

IGVAW YQQKP GQSPK LLIYS ASSRY TGVPD RFSGS GSGTD FTFTI SSVQA  100

EDLAV YYCQQ HYTSP FTFGS GTKLE IK                             127
```

FIGURE 16



JO79 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GATATCCACC ATGAAATGCA GCTGGGTCAT TCTCTTCCTC CTGTCAGGAA    50
CTGCAGGT                                                  58
```

JO80 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GCTAGCTGAG GAGACGGTGA CCAGGGTTCC TTGACCCCAA TAGTCCATAG    50
TATATCT                                                   57
```

JO82 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TAAGTCCAAT CCACTCAAGG TTCATTCCAG GGCTCTGCTT CACCCAGTGC    50
ATGGTATAGC CAGTGAATGA GTAACCAGAA GCCTTGCAGG AGACCTTCAC   100
```

JO83 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GATTGGACTT ATTAATCCTT ACAATGGTGG TACTGTCTAC AACCAGAAGT    50
TCCAGGACAA GGCCACATTA ACTGTAGACA AGTCAACGAG CACAGCCTAC   100
```

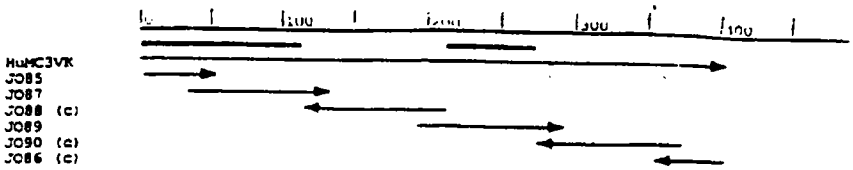
JO84 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
CAATAGTCCA TAGTATATCT CCAACGTCTT GCACAGAAAT AGACTGCCGT    50
GTCCTCAGAT CTCAGACTGC TGAGCTCCAT GTAGGCTGTG CTGGTTGACT   100
```

JO81 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TCCTGTCAGG AACTGCAGGT GTCCACTCTG AGGTCCAGCT GGTGCAGTCT    50
CGAGCTGAGG TGAAGAAGCC TGGAGCTTCA GTGAAGGTCT CCTGCAAGGC   100
```

FIGURE 17



JO85 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GATATCCACC ATGGAGTTCC AGACCCAGGT CTTTGTATTC GTGTTTCTCT    50
GG                                                        52
```

JO86 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
gtcgacTTAC GTTTTATTTC CACCTTTGTC CCCGAGCCGA ACGTGAATGG    50
```

JO87 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TTGTATTCGT GTTTCTCTGG TTGTCTGGTG TTGACGGAGA CATTGTGATG    50
ACCCAGTCTC CAGACTCCCT GGCTGTGTCA CTGGGAGAGA GGGCCACCAT    100
```

JO88 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TCAGCAGTTT AGGAGATTGT CCTGGTTTCT GTTGATACCA GGCTACACCA    50
ATACTCACAT CCTGACTGGC CTTGCAGGTG ATGGTGGCCC TCTCTCCCAG    100
```

JO89 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
ACAATCTCCT AAACTGCTGA TTTACTGGGC ATCCTCCCGG TACACTGGAG    50
TCCCTGATCG CTTCAGTGGC AGTGGATCTG GGACGGATTT CACTCTCACC    100
```

JO90 Sequence

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
CCCGAGCCGA ACGTGAATGG AGAAGTATAA TGTTGCTGAC AGTAATAAAC    50
TGCCACGTCT TCAGCCTGCA GACTGCTGAT GGTGAGAGTG AAATCCGTCC    100
```

Figure 18: HuMc3 V_H (BR-M version)

Fig. 18A

```
--g ata tcc acc ATG AAA TGC AGC TGG GTC ATT CTC TTC CTC CTG TCA GGA   49

ACT GCA GGT GTC CAC TCT GAG GTC CAG CTG GTG CAG TCT GGA GCT GAG GTG  100

AAG AAG CCT GGA GCT TCA GTG AAG GTC TCC TGC AAG GCT TCT GGT TAC TCA  151

TTC ACT GGC TAT ACC ATG CAC TGG GTG AAG CAG AGC CCT GGA ATG AAC CTT  202

GAG TGG ATT GGA CTT ATT AAT CCT TAC AAT GGT GGT ACT GTC TAC AAC CAG  253

AAG TTC CAG GAC AAG GCC ACA TTA ACT GTA GAC AAG TCA ACG AGC ACA GCC  304

TAC ATG GAG CTC AGC AGT CTG AGA TCT GAG GAC ACG GCA GTC TAT TTC TGT  355

GCA AGA CGT TGG AGA TAT ACT ATG GAC TAT TGG GGT CAA GGA ACC CTG GTC  406

ACC GTC TCC TCA gct agc                                              424
```

Fig. 18B

```
MKCSW VILFL LSGTA GVHSE VQLVQ SGAEV KKPGA SVKVS CKASG YSFTG   50

YTMHW VKQSP GMNLE WIGLI NPYNG GTVYN QKFQD KATLT VDKST STAYM  100

ELSSL RSEDT AVYFC ARRWR YTMDY WGQGT LVTVS S                  136
```

Figure 19: HuMc3 V_K (BR-M version)

Fig. 19A

```
--g ata tcc acc ATG GAG TTC CAG ACC CAG GTC TTT GTA TTC GTG TTT CTC   49

TGG TTG TCT GGT GTT GAC GGA GAC ATT GTG ATG ACC CAG TCT CCA GAC TCC  100

CTG GCT GTG TCA CTG GGA GAG AGG GCC ACC ATC ACC TGC AAG GCC AGT CAG  151

GAT GTG AGT ATT GGT GTA GCC TGG TAT CAA CAG AAA CCA GGA CAA TCT CCT  202

AAA CTG CTG ATT TAC TCG GCA TCC TCC CGG TAC ACT GGA GTC CCT GAT CGC  253

TTC AGT GGC AGT GGA TCT GGG ACG GAT TTC ACT CTC ACC ATC AGC AGT CTG  304

CAG GCT GAA GAC GTG GCA GTT TAT TAC TGT CAG CAA CAT TAT ACT TCT CCA  355

TTC ACG TTC GGC TCG GGG ACA AAG GTG GAA ATA AAA cgt aag tcg ac       404
```

Fig. 19B

```
MEFQT QVFVF VFLWL SGVDG DIVMT QSPDS LAVSL GERAT ITCKA SQDVS    50

IGVAW YQQKP GQSPK LLIYS ASSRY TGVPD RFSGS GSGTD FTLTI SSLQA    100

EDVAV YYCQQ HYTSP FTFGS GTKVE IK                               127
```

Figure 20

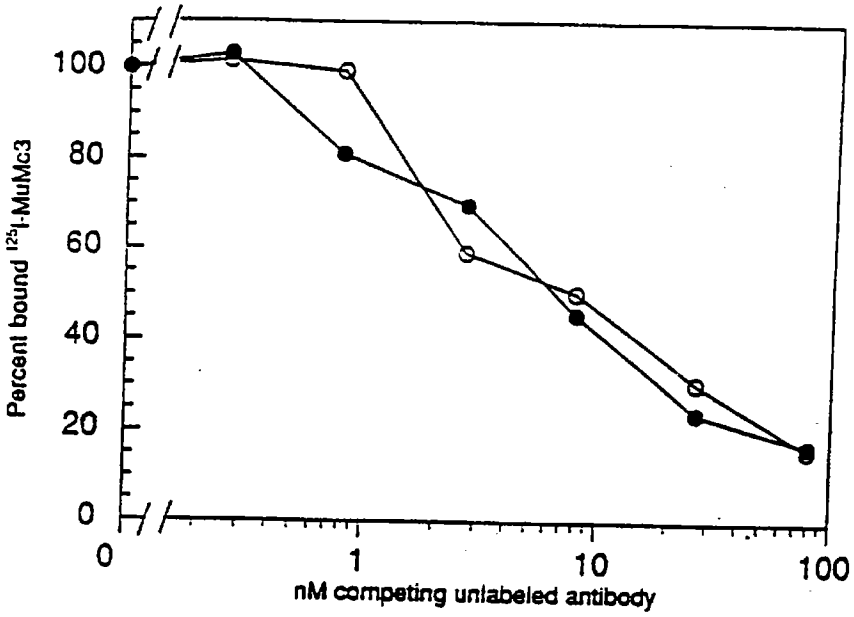

100
80
60
40
20
0
0
1
10
100
Percent bound ^{125}I-MuMc3
nM competing unlabeled antibody

Figure 21

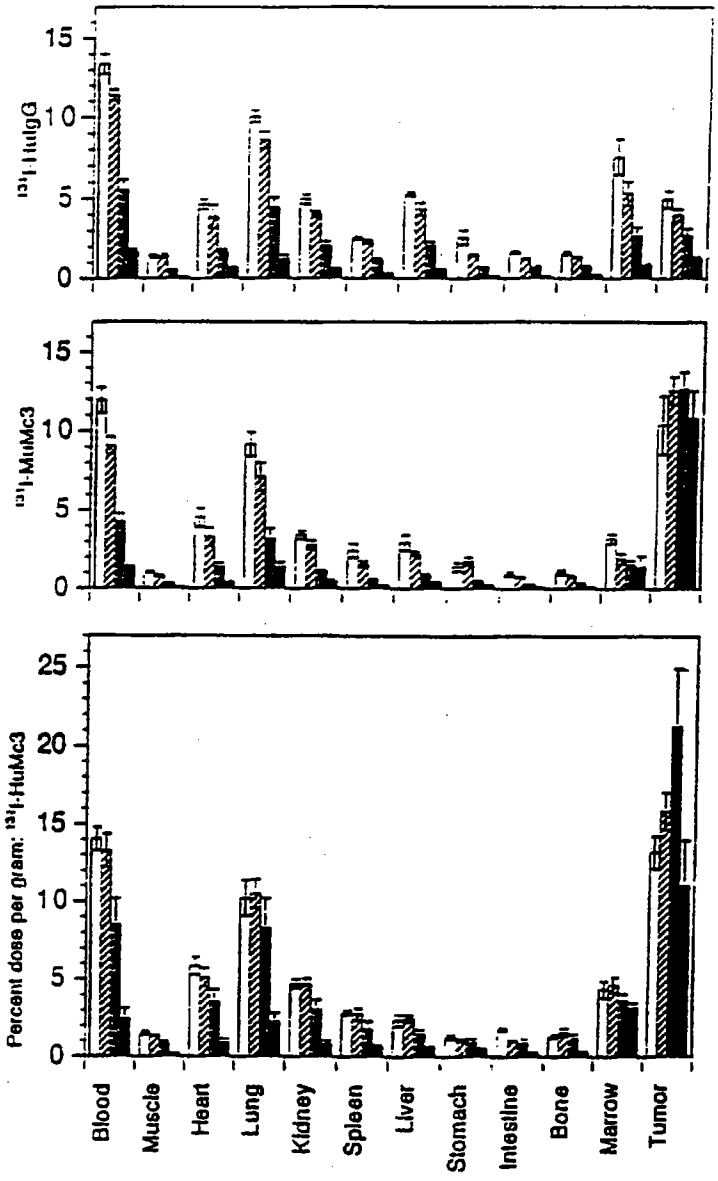

15
10
5
0
^{131}I-HuIgG
15
10
5
0
^{131}I-MuMc3
25
20
15
10
5
0
Percent dose per gram: ^{131}I-HuMc3
Blood
Muscle
Heart
Lung
Kidney
Spleen
Liver
Stomach
Intestine
Bone
Marrow
Tumor

Figure 22

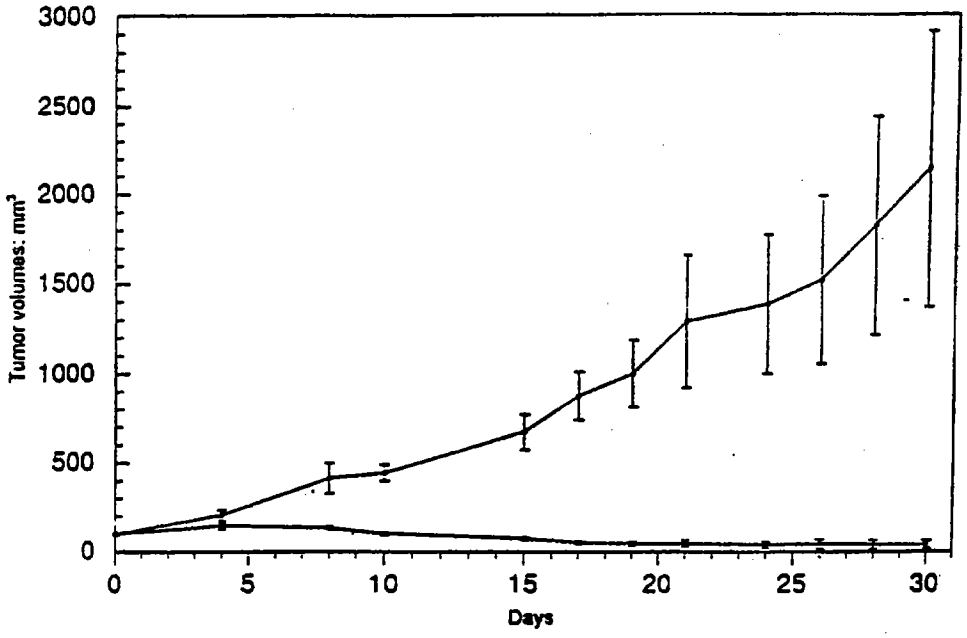
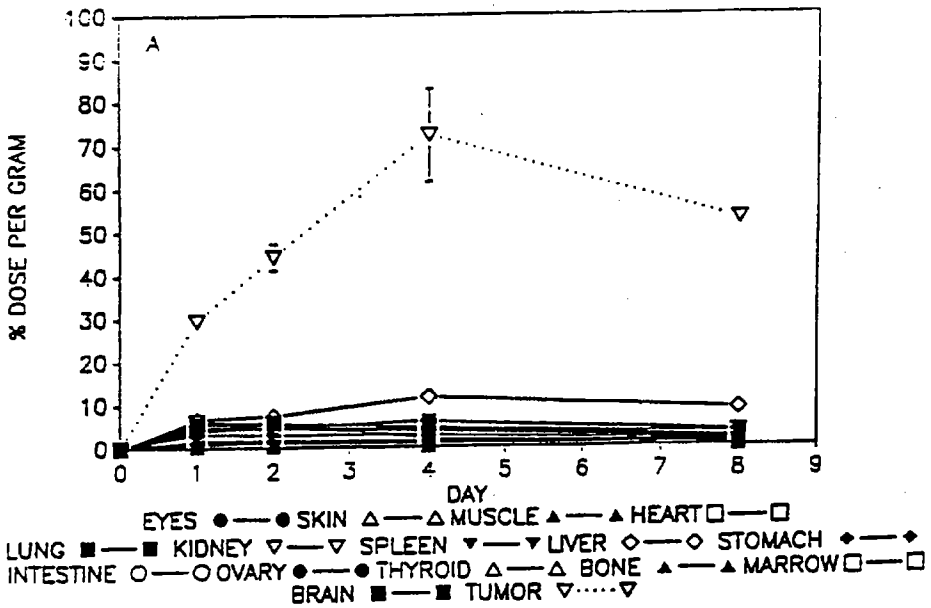
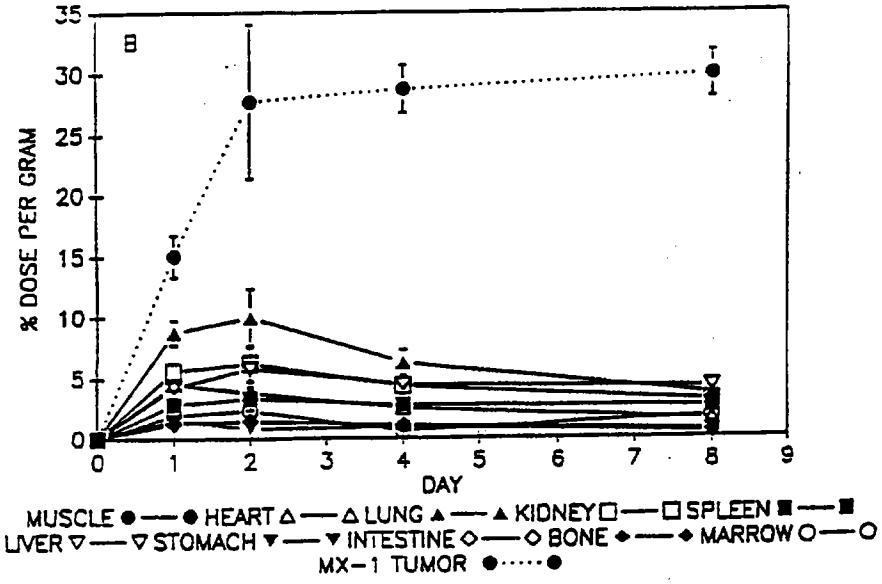

3000
2500
2000
1500
1000
500
0
Tumor volumes: mm³
0
5
10
15
20
25
30
Days

Figure 23


A
% DOSE PER GRAM
DAY
EYES
SKIN
MUSCLE
HEART
LUNG
KIDNEY
SPLEEN
LIVER
STOMACH
INTESTINE
OVARY
THYROID
BONE
MARROW
BRAIN
TUMOR


B
% DOSE PER GRAM
DAY
MUSCLE
HEART
LUNG
KIDNEY
SPLEEN
LIVER
STOMACH
INTESTINE
BONE
MARROW
MX-1 TUMOR